46, Appl 11, Appl 8, Appli 331, App

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Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                        Sequence
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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US-08-742-113
US-09-175-928-31
US-08-858-207A-113
PCT-US95-10668-3
PCT-US95-10668-4
US-09-236-097-11
US-09-236-097-11
US-09-236-097-11
US-09-256-315-82
US-09-265-315-82
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100.0%; Pred. No. v, ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36, 373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
           version 4.5
- 2000 Compugen Ltd.
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US-08-41-435-5
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US-08-73-637B-27
US-08-526-840B-27
US-08-726-440B-27
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US-08-731-716-1
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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61 TGCCCAAGCTAATGATATTCCC	61 TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACA 1 121 TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 1	121 TCGCTTCTTCGACCACAGGGGG 181 TCTGCAAAGCAATTCCTCCAA 181 TCTGCAAAGCAATTCCTCCAA	241 TACTTTTCAACTTCCACCACCACACTATTCTCGTAAGGCTCAGGAAGCTTGGTT 241 TACTTTTCAACTTCCACCACCACACTATTTTTCTCGTAAGGCTCAGGAAGCTTGGTT 241 TACTTTTCAACTTCCACCTTCCGACGAGACTATTTTTTCTCGTAAGGCTCAGGAAGCTTGGTT 241 TACTTTTCAACTTCGACCACACACTACTACACACTTTGGTT	301 AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAATCTTGACCTACTATATAAATAA	361 GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCTCAAAACTACTATGGTAA 	421 AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	481 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCGGAAACTTGGTCTT 540	541 ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAGCAGTCAATAC 	601 ACCAATTACTGATGGACTACAAAGTCTGCAAGTAATTACCCTGCTTACATGGA	661 TAATTACCTCAAGGAAGTCATCAATCTGAAGAAGAAAGAA	721 AACTGGGATGGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT 780 	781. TTACAATACAGAGGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 84	841 IGTTGATGTTTCTAACGGTAAAGTCATGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA 	901 TGTTTCCTTCGGAATTAACCAGGCAGTAGAAACAAACCGCGACTGGGGATCAATGAA 960 	961 ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT 1020	1021 CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG 1080 	1081 GGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC 1140 
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TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATGAA 1007
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  CAAAAAATATGGAGCAAGTAAGTGAAAAGATGGCTGCTGCTTACGTTTGCAAATGG
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                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 0;
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                                                                                                                                                                                                                                                                    NAME: STEFFIEL TRICHARD J.

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-151

TELEPHONE: (212) 819-8783

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: PCR cloning
CLONE: pARC 0512 Soluble PBP 1A del
                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWHER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.18;
99.48;
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ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2049 base pairs
TYPE: nucleic acid
            : New York
RY: United States
10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.1
Best Local Similarity 99.4
Matches 1988; Conservative
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                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LOCATION: 1..2049
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IMMEDIATE SOURCE:
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CITY: Nev
STATE: NE
COUNTRY:
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US-08-481-435-5
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                                                                          TTCTACGTGGAACTCACCTGCTCCACAACACCCCCATCAACTGAAAGTTCAAGCTCATC 1860
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                                                                                                                   TIGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG
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APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08245511
Patent No. 5928900
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                  600-1-069 CIP
                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae
                                           REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELERAX: 201 487-5800
TELERAX: 201 343-1664
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.77
Matches 946; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 1..960
US-08-245-511-3
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HYPOTHETICAL: NO
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                                                                                                                                        781 TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 840
851
                                                                                                   901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGA 949
                                                                                                                                                                                                                                                       APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Promanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/600,993A FILING DATE: 1-MAR-1996 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/245,511 FILING DATE: 18-MAY-1994 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/116,541 FILING DATE: 01-SEP-1994 ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 600-1-069
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: All Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08600993A Patent No. 5981229 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                 Length 960;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                 Query Match 47.2%; Score 944.2; DB 2; Best Local Similarity 99.7%; Pred. No. 1.9e-278; Matches 946; Conservative 0; Mismatches 3;
                               ORGANISM: Streptococcus pneumoniae
                                               STRAIN: R6
IMMEDIATE SOURCE:
CLONE: SPRU42
                                                                                                               NAME/KEY: CDS
LOCATION: 1..
ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                  US-08-600-993A-3
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBLOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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  142 GATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAATCTGCAAA---GCAATTCCCT 198
                                               ATTAGACCCTATCGGCATTGCCCGTGCATTGTTTGTCGCAGTGAGTAATGGCGGTGCATC
                                                                                                                       TTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTTAGCGATTCAGTTAGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
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ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
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Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
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TITLE OF INVENTION: SPECI
TITLE OF INVENTION: AMPLI
TITLE OF INVENTION: COMMO
TITLE OF INVENTION: FROM
NUMBER OF SEQUENCES: 177
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COMPUTER READABLE FORM:
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APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELETTE, Marc
APPLICANT: OUELETTE, Marc
APPLICANT: OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: DEBTECT AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: DEBTECT AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: DEBTECT AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
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841 TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA 900
                                          852 TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA 911
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                                                                                                                912 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGA 960
                                                                                        901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGA 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 850586.90012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZUP: 53.20.4497
ZUP: 53.20.24497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Data:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04.NOV-1996
CLASSIFFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11.SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAST WISCONSIN AVENUE
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REGISTRATION NUMBER: 35,433
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TELEPHONE: (414) 277-5000
TELEPAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 27:
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LENGTH: 9100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
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US-08-743-637B-27
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US-08-481-435-1
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                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                  Length 9100;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                Query Match 5.9%; Score 117.2; DB 3; Best Local Similarity 50.3%; Pred. No. 2e-25; Matches 349; Conservative 0; Mismatches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCGTCTTTTGGCGAAGAAAATGCTTACACC 2814
            NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35 433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                679 CATCAATCAAGTTGAAGAAGAACAGGCTATAAC 712
                                                                                                                                                                                                                       ORIGINAL SOURCE: ORGANISM: Haemophilus influenzae US-08-526-8408-27
                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                   linear
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
Sequence 1, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 3;
Pred. No. 6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : PCR cloning
pARC 0558 Soluble PBP 1A del 23
                                                                                                                                                                      ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-153
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2487 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 290; Conservative
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STRANDEDNESS: double
                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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LIBRARY: PCR C
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; LOCATION:
US-08-481-435-1
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                      483 ACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTTAT 542
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                                                                                                                                                        320 TCTTCCTCAGTCC----AGAACGCACGCTGATGCGTAAGATTAAGGAAGTCTTCCTCG 373
                                                                                                                                                                                                                                                                                                                                                                                           494 CGGTCGACCAACTGACGCTGAACGAATGGCGGTGATAGCCGGGCTGCCGAAAGCGCCTT 553
                                                                                                                                                                                                CGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAAGG
                                      TGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGACTT
                                                                           260 TGTTCTCCGGTCACGCGTCACAAGGGGCAAGTACCATTACCCAGCAGCTGGCGAGAAACT
                                                                                                                 243 ACTITICAACTICGACTICCGACCAGACTATITCICGTAAGGCTCAGGAAGCTIGGITAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08771716
Patent No. 5922540
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Hoskins, Joan
APPLICANT: Hoskins, Joan
APPLICANT: Statud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase
TITLE OF INVENTION: Gene of Staphylococcus Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 46285

ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Webster, Thomas D.
REGISTRATION UNDRER: 39,872
REFERENCE/DOCKET UNDRER: X-11
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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nucleic acid
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STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                  Length 807;
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APPLICANT: Hoskins, Joann
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Gene of Staphylococcus Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                Score 62.2; DB 2;
Pred. No. 3.4e-09;
0; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 CAATAATTTAAGTTTACCTCAGT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08771716
Patent No. 5922540
                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                  3.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603 GAATAAAATAGTACAACAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Lilly Corporter: Indianapolis STATE: Indiana
                                                                                                                                               1..807
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Peery,
                                                                                  ANTI-SENSE: NO FEATURE:
                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                   US-08-771-716-1
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                                                                                                                                                                                                                                    Query Match
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67 AGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 CTTCGACCACAGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAATCTGCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09057720A
Patent No. 6143866
GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: Hoskins, John
APPLICANT: Askunas, S.Richard
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase Gene
TITLE OF INVENTION: of Staphylococcus Aureus
NUMBER OF SEQUENCES: 3
         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.2; DB 3; 1
Pred. No. 3.4e-09;
0; Mismatches 183;
                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOOKET NUMBER: x-11067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYRENT 807 base pairs
TYRENT 807 base pairs
TYRENT 807 base pairs
TYRENT 100FOLGY: linear
                                          US/09/057,720A
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                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.9
Matches 191; Conservative
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                                       APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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Patent No. 6143868
GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: Hoskins, Joann
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase Gene
TITLE OF INVENTION: of Staphylococcus Aureus
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        Length 807;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                        3.1%; Score 62.2; DB 2; 133.9%; Pred. No. 3.4e-09; ive 61; Mismatches 183;
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-11067
TELECOMMULICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.9%
Matches 130; Conservative
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                                                                                                                                                                                                  MOLECULE TYPE: mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-08-771-716-3
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US-09-057-720A-1
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Gaps

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Length 807; Indels 426

366

Protein From

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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,716
APPLICANT: Zhao, Genshi
APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: No. 5789202ris, Franklin H.
ATTLE OF INVENTION: Penicillin Binding Protei
                                                                                              STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                         x-10,887
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: 317-276-3334 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                         ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGETH: 2193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 381; Conservative
                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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FEATURE:
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                                                                                                                                                                                            COUNTRY:
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                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1%; Score 62.2; DB 3; Best Local Similarity 33.9%; Pred. No. 3.4e-09;
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US-08-731-716-1
; Sequence 1, Application US/08731716
; Patent No. 5789202
; GENERAL INFORMATION:
APPLICAMT: HOSKINS, JOANN
; APPLICANT: ROSKOS, S. Richard
; APPLICANT: ROCKOS, Pamela K.
     Lilly Corporate Center
                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEBSIEF, THOMES D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-110
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                 ZIP: 46285
COMPUTER READABLE FORM:
                     Indianapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                        Indiana
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                                                                                                                                                                                                            FILING DATE:
                                                     COUNTRY:
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Length 2193;
                                                                      0; Mismatches 446;
2.8%; Score 56.4; DB 1; 44.6%; Pred. No. 3.4e-07;
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625 TATTTTGGAAATGGTGTGTGGGGTGTAGAAGATGCGAGTAAGAAATACTTTGGAGTTTCT 684
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                                CAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCGGAAACTTGGTCTTATCT
                                                                                                                                      745 CTGTATAATCCCTTGAATTCCGTAGAAGATTCTACTAATCGGCGCGATACTGTCTTGCAG
                                                                                                                                                                           GAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATACACCA
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APPLICANT: Hoskins, Joann
APPLICANT: Hoskins, Joann
APPLICANT: Bockey, Pannela K.
APPLICANT: Zhao, Genshi
APPLICANT: Rockeck, Paul R. Jr.
APPLICANT: Rockeck, Paul R. Jr.
APPLICANT: Property, Penicillin Binding Protein From TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SUGUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: X-10,887
TELECOMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Eli Lilly and Company
F: Lilly Corporate Center
Indianapolis
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Patent No. 5789202
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GUCAAUAAUGGCUACCGCAUUUACACAGAGCGGGACCAAAAACUACCAAGCAAAUGUGCGG 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 UUCUAUAAAAUGACGGGAUUAACUAUGGCCGUUUC------UUCUUGGCUAUUGUC 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCAACTTCGACTTCCGACCAGACTATTCTCGTAAGGCTCAGGAAGCTTGGTTAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 UVAGAAUUAAGCAAAAAUAUAGUAAGGAGCAAAUUCUAACCAUGUACCUUAACAACGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTTATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUGACUUCGCAAUUGCACGAUAAGUAUGAAGGAAAAAUCUCAGAUUACCGUUACCCUCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCTCAAGGAAGTCATCAATCAAGTTG.....AAGAAGAAACAGGCTATAACCTA
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                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                    Length 2193;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  Query Match 2.8%; Score 56.4; DB 1; Sest Local Similarity 31.6%; Pred. No. 3.4e-07; Matches 270; Conservative 111; Mismatches 446;
2193 base pairs
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                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                    TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYDOTURETY
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                                                                                               HYPOTHETICAL: N
HYPOTHETICAL: NO
HATI-SENSE: NO
US-08-731-716-3
LENGTH:
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TYPE: DNA
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    Sequence 206, Application US/09060756

Patent No. 6183957

GENERAL INFORMATION:
APPLICANT: COLe. Stewart
APPLICANT: Gordon, Stephen
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Blain
APPLICANT: BLAND WETHOR FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 206
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; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-206
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Patent No. 6339174
GENERAL INFORMATION:
APPLICANT: STRAUSS, ANDREAS
APPLICANT: THUMM, GUNTHER
APPLICANT: POHLMER, JOHANNES
APPLICANT: GOTZ, FRIEDRICH
TITLE OF INVENTION: METHOD FOR IDENTIFYING A NUCLEIC ACID
FILE REFERENCE: 10496/P65266US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/508,542
CURRENT FILING DATE: 2000-05-16
PRIOR PRICATION NUMBER: PCT/EP98/06136
PRIOR FILING DATE: 1998-09-26
PRIOR PLICATION NUMBER: 97 116 841.4
PRIOR PLING DATE: 1997-09-27
PRIOR APPLICATION NUMBER: 97 118 755.4
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
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US-09-060-756-206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1462 TTATGGAACTGGACGAAATGCCTATCTTGCTTGGCTCCCTCAGGCTGGTAAAACAGGAAC 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1285 AAAGATGGCTGCTTACGCTGCCTTTGCAAATGGTGGAACTTACTATAAACCAATGTA 1344
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                                                                                                                                                                                                                                                                                                       g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Score 53.8; DB.4; Length 1474; 50.4%; Pred. No. 1.7e-06; tive 0; Mismatches 174; Indels 6
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LOCATION: (1)..(1474)

COTHER INFORMATION: "n" represents a, t,

US-09-508-542-17
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Job time: 4168 sec
                                                                                                                                                                                 ORGANISM: Staphylococcus carnosus FEATURE:
PRIOR FILING DATE: 1997-10-29
                         NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 1474
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.4<sup>§</sup>
Matches 183; Conservative
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1999
1 TAAAATCTACGACAATAAAA......ATCCTCAACCAGCACAACCA 1999
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                                                                                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
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57: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
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60: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
60: /cgn2_6/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Description	edneuc edneuc	Sequence 81, Appl Sequence 145, App Sequence 1312, Ap	932	9325,	Sequence 596, App Sequence 3, Appli	139, A e 139,	Sequence 139,	6631, 6631,	6631,	÷.	equence 217,	Sequence 2013, Ap Sequence 2013, Ap	equence 91, A	ednence	eduence 495,	equence 710,	equence 44, A	e 14, A	
ID	-09-536-784-1 -09-765-271-1 -09-765-272-1	029-960-81 961-527-145 583-110-131	1-107- 302-03	72-851-932 01-998-596	)-068-175-59 :116-541-3	-14436-13 11-503-13	11-503A-13	:-03 115-	72-851-663	.34-000-153 )70-927-217	70-927A-21	.07-532-20 .07-532A-2	91-007-91	S-60-068-186-4	S-60-050-444-49	60-068-217-71	S-09-634-238-4	-09-634-238-14	-045-649-
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/cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:

273 13.7 933 43 US-60-046-653-183 Sequence 183, App 221.4 11.1 6394 26 US-09-663-779-1130 Sequence 1130, Ap 221.4 11.1 6394 26 US-09-663-779-1130 Sequence 1130, Ap 204 12.2 US-09-683-779-1131 Sequence 1131, Ap 204 12.2 US-09-583-110-1313 Sequence 1131, Ap 2123 8 G.2 2229 36 US-09-974-300-11671 Sequence 1671, Ap 2123.8 G.2 1899 24 US-09-620-608-1543 Sequence 1543, Ap 2123.8 G.2 1899 53 US-60-1444-883-1543 Sequence 1543, Ap 2122.8 G.1 1590 42 US-60-038-697-335 Sequence 2090, Ap 2122.8 G.1 1590 43 US-60-046-714-308 Sequence 318, App 2120.6 G.0 2181 1 US-09-815-242-4727 Sequence 4727, Ap 2120.6 G.0 2181 37 US-10-072-851-4727 Sequence 4727, Ap 2120.6 G.0 2181 37 US-10-072-851-4727	ALIGNMENTS  SEQUENCE (LASTRAIN)  SEQUENCE (LASTRAIN)  SEQUENCE (LASTRAIN)  SEQUENCE (LASTRAIN)  SEQUENCE (LASTRAIN)  STREET: 9410 Key West Avenue  CORRESSEN: Human Genome Sciences, Inc.  STREET: 9410 Key West Avenue  CORPTER EXABALE FORM:  WEDINH TYPE: DISKETE, 3,50 Inch, 1.4Mb storage  COMPTER: Maryland  SOFTER: Maryland  COMPTER: Maryland  COMPTER: Maryland  COMPTER: Maryland  COMPTER: Maryland  COMPTER: Maryland  COMPTER: Maryland  SOFTER: Maryland  COMPTER: Maryland  FELENROMORICATION NUMBER: D8340P3  FELENROMORICATION NUMBER: P8340P3  FELENROMORICATION NUMBER: Marks  REGISTRATION	Match
0000 EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	RESULT 1 US-09-536-784-1 Sequence 1, A Sequence 1, A SEARES ITILE NUMBER CORRES CORRES CORRES CORRES COMPUT TO C C C C C C C C C C C C C C C C C C C	Query Match Best Local Matches 199 Oy 1 TAA Oy 61 TGC Oy 61 TGC

1080 1140 1020 .1200 240 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 660 720 180 240 300 480 480 540 540 780 780 840 840 900 960 180 300 360 360 420 420 009 600 720 900 960 TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAAAAACGGCTATAACCTACTCAC TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGCGACTGGGGGATCAACTATGAA TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCCAACAGTTGATTAAGTTGAC TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCCAAGACCGCCGAAACTTGGTCTT AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 121 241 301 541 841 1021 1081 1081 1141 181 181 241 301 361 421 421 481 541 601 661 661 721 781 781 961 1021 1141 121 361 481 601 721 841 901 901 961 q 셤 g g g g q qq q g g g g Db ò ò Ω δý δý οy Q δ οy Qγ οy ò ò ò q Q В ò Qγ g δý g

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0; Mismatches
                                             APPLICATION NUMBER: US/09/765,271
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1999; 100.0%; Pred. No. 0;
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/536,784
FILING DATE: <UNKNOWN-
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHALLE S. MARKS
REGISTRATION NUMBER: 41,971
          OPERATING SYSTEM: MSDOS Version
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                         pairs
                                                                                                                                                                                                                                                                              STRANDEDNESS: double
 HP Vectra
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                      LENGTH: 1999 base
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Matches 1999; Conserv
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                                                                                           CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTGCTTACGCTGCCTTTGCAAATGG
                                                                                                                                           AGAGTICICTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGA
                                                                                                                                                                                          GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
TILLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
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STATE: Maryland
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  Sequence 1, Application US/09765272 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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ilarity 100.0%;
Conservative 0;
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Matches 1999; Conser
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <ur>
CHASSIFICATION ON SURROWN>
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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FILING DATE: <Unknown>
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R OF SEQUENCES: 1649
SPONDENCE ADDRESS:
RESSEE: Human Genome Sciences,
SET: 9410 Key West Avenue
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                          COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
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                                                                                                                                                              REGISTATION NUMBER: B1373
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 10383 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/029,960
FILING DATE:
                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION
                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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Pred. No. 0;
; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                              Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/961,527
                                                                                                                                                                                                                                                                                                                                  Sequence 145, Application US/08961527
GENERAL INFORMATION:
APPLICANT: Charles Unsch
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Pred. No. 0;
0; Mismatches
   US 09/107,433
                    60/085,131
                                                                                            pneumoniae
PRIOR APPLICATION NUMBER: US US US PRIOR FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/C PRIOR FILING DATE: 1998-05-12 PRIOR FILING DATE: 1998-07-02 PRIOR FILING DATE: 1997-07-02 PRIOR FILING DATE: 1997-07-05 NUMBER OS EQ ID NOS: 5322 SEQ ID NO 1312
                                                                                                                             99.4%;
ilarity 99.6%;
Conservative
                                                                                           ; ORGANISM: Streptococcus
US-09-583-110-1312
                                                                                                                             Query Match
Best Local Similarity
Matches 1992; Conserv
                                                                                  TYPE: DNA ORGANISM:
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                                                                                                                                                                                                                                     Sequence 1312, Application US/09583110
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pueumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
                   GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
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                                                                                                                                                                                           Sequence 1102, Application US/09107433
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A DOUCETTE-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
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APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
FILING DATE: July 2, 1997
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larity 99.6%; Pred. No. 0;
Conservative 0; Mismatches
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LOCATION: (B) LOCATION 1...2166
SEQUENCE DESCRIPTION: SEQ ID NO: 1102:
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <UNKnown>
OPERATING SYSTEM: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1102:
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TYPE: nucleic acid
STRANDEDNESS: double
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ULE TYPE: DNA (genomic)
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STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity
Matches 1992; Conserv
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1740 1500 1560 1724 1844 1860 2024 2144 **AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACACCGAATCAGA** CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTGCTTACGCTGCTTTGCAAATGG TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA **TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA** GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG TACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGAA 2163 TCCTCAACCAGCACAACCA 1999 TCCTCAACCAGCACAACCA 1365 1545 1605 1741 2025 2085 1201 1261 1425 1321 1485 1381 1441 1501 1665 1561 1725 1621 1785 1681 1905 1801 1965 1861 1921 1981 2145 q g Q Dp g Op qq Dp g d 셤 g g q Qγ δý δ Ω ò Ω ôγ Ω Q ò õ ŏ òγ

a Compound the Target of JULIANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SCOFTRARE: FastSEQ for Windows Version 4.0 RESULT 8
PCT-US02-03987-9325
SCT-US02-03987-9325
GENERAL INFORMATION:

SOFTWARE: SEQ ID NO 9

which Inhibit

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                                                    Score 1981.4;
Pred. No. 0;
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                                                          Best Local Similarity 99.4
Matches 1988; Conservative
           ORGANISM: Streptococcus
                      NAME/KEY: CDS
LOCATION: (1)...(2160)
USO2-03987-9325
2160
                                                    Match
     TYPE: DNA
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Pred. No. 0;
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                                                  Sequence 9325, Application US/09815242 GENERAL INFORMATION:
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                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
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Best Local Similarity 99.4%;
Matches 1988; Conservative.
                                                                   APPLICANT: Haselbeck, Robert
        tcctcaaccagcacaacca
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                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)...(2160)
US-09-815-242-9325
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Best Local Similarity 99.4
Matches 1988; Conservative
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2160)
US-10-072-851-9325
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APPLICANT: FOLIANS; O'SOLOUI
APPLICANT: Haselbeck, Robert
APPLICANT: O'SISAN, Kari L.
APPLICANT: O'SSKING, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Roemer, Terry
APPLICANT: Boone, Charles
APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
TITLE TILE TILE TILE OF INVENTION: WINBER: US/10/072,851
CURRENT APPLICATION NUMBER: US/10/072,851
         GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT 1620
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                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Goordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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LENGTH: 2160
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APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AM. L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGORY L.
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
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RESULT 11
US-60-061-998-596/c
; Sequence 596, Application US/60061998
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORREY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTATION UNMBER: 39,132
REFERENCE/TOOKET NUMBER: PM-00
TELECOMMUNICATION INFORMATION:
TELEFONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 1988; Conservative
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: SPNIC601
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CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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91   ACCORTICACTINGACOMACCINACIONAGUMICTICACCTICATINITAMINI   3159     94   94   ACCORTICACTINGACOMACCINACIONAGUMICTICACCTICATINITAMINI   3159     95   95   97   97   97   97   97   97	Db 8338 AGAGTTCTCTAATGTCGGAACTCGTGCCATGAA	Oy 1441 CATGATGAAACAGTCTTGACTTATGGAACTGG	Qy 1501 TCAGGCTGGTAAAACAGGAACCTCTAACTATAC	Qy 1561 GACCTCTCAATTTGTAGCACCTGATGAACTATT	1621		1741	1801	1861	1921 TACCAATCCTAACATATACGC 	Oy 1981 TCCTCAACCAGAGCA 1999 111111111111111111111111111111111	RESULT 12 US-60-068-175-596/c ; Sequence 596, Application US/60068175	GENERAL INFORMATION: APPLICANT: Lagace, Robert E. APPLICANT: Corley, Neil C. APPLICANT: Russo, Frank D.	APPLICANT: Hanh, Amy L. ; APPLICANT: Heath, Joe D. ; APPLICANT: Finney, Gregory L. ; TITLE OF INVENTION: NUCLEOTIDE SEQUEN	TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: INCYTE	STREET: CITY: PA STATE: C COUNTRY:	COMPUTER REAL MEDIUM TYPE	CURRENT APPLICATION DATA:  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/60/068,175	CLASSIFICATIO
	301 AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAATAA	361 GGTCTACATGTCTAATGGGAACTATGGAATGCAGACACGGCTCAAAACTACTATGGTAA 	421 AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	481 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT 540	541 ATCTGAAATGAAAAACCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC 600	601 ACCAATTACTGATGGACTACAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA	661 TAATTACCTCAAGGAAGTCATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC 720 	721 AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT 780 [	781 TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAAGTGCAAGTCGCTTCTACCAT 840	841 IGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTAA 900	901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACCGCGACCGGGGATCAACTATGAA 960 	961 ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT	1021 CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG 	1081 GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC	1141 CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAGG	1201 AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA 	1261 CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTACGCTGCCTGTTTGCAAATGG 132	1321 TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAA 138 	1381 AGAGTECTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGGA 144
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                    TTTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCA
                                       TCTACAACTCCGATCAATACGTCTTTACCCTGACGATGATTTGCAAGTCGCATCTACGG
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                                                                                                                                                                                               Length 9845;
                                                                                                                                                                                                                  223; Indels
                                                                                                                                                                                               DB 45;
                                                                                                                                                                                             Score 1631.2;
Pred. No. 0;
0; Mismatches
     NAME: CERRONE, MICHEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0009-2 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-416
INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
LENGTH: 9845 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 9845 base pairs
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
INMEDIATE SOURCE:
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                                                                                                                                                                                             81.6%;
88.8%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             Query Match
Best Local Similarity 88.8'
Matches 1776; Conservative
                                                                                                                                                     ; CLONE: SPN2C598
US-60-068-175-596
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          APPLICANT: Masure, H. Robert
APPLICANT: Pearce, Barbara J.
APPLICANT: Poumanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,541
FILING DATE: 19930901
CLASSIFICATION: 424
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R6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATORNEY AGENT INFORMATION:
NAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
                                                                                                                                                        US-08-116-541-3; Sequence 3, Application US/08116541; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      411 Hackensack Avenue
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                                                                                                   1980 ATCCTCAACCAGCACCA 1999
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 99.7
Matches 946; Conservative
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CLONE: SPRU42
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ORIGINAL SOURCE:
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STRAIN: R
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US-08-116-541-3
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Length 960; Indels

Score 944.2; DB 5; Pred. No. 1e-256; 0; Mismatches 3;

47.28; 99.78;

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                                                                                                                                                                                                                                                                                601 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA
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                                   TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA
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GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richard
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Knowles, David
Lonetto, Michael
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1593 TTGCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTCTAACCGTCTGA
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                           781 ATACAACCCTGATCAACAAATCAGAATCCTCAACCAGCACAACCA 827
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APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richael
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 713
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,503
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 139, Application US/08911503 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICOR APPLICATION DATA:
APPLICATION NUMBER: 60/024
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glimit, EGWARG R
REGISTRATION NUMBER: 38,89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2172 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 709 Swedeland CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
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                    TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES, TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
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Pred. No. 5.1e-218;
0; Mismatches 4;
                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASLSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/14436
FILING DATE: 15-AUG-1997
                                                                                                 ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
Robert
NOVEL PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P50533
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
FILING DATE: 16-AUG-1996
ATTORNEY AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 139:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pairs
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Best Local Similarity 99.49
Matches 822; Conservative
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
                                                               NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                       STATE: P. COUNTRY:
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                                                                              4; Indels
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Pred. No. 5.1e-218;
                                                                              0; Mismatches
                                                        40.5%;
; STRANDEDNESS: single
TOPOLGGY: linear
; MCLECULE TYPE: Genomic DNA
US-08-911-503-139
                                                        Query Match
Best Local Similarity 99.4'
Matches 822; Conservative
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Search completed: June 13, 2002, 14:43:46 Job time: 7603 sec

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Seguence 438, Seguence 438,

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Run on:

Scoring table:

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Sequence 438, Sequence 438, Sequence 438,

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Sequence 1, Application US/08961083
GENERAL INFORMATION:
APPLICANT: Chol et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 60
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,083

FILING DATE: 30-Oct-1997

CLASSIFICATION: CURKNOWN>
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                                                        US-10-027-632-235624

US-60-360-039-32748

US-10-027-639-214424

US-10-027-632-219980

US-10-123-155-438

US-10-113-155-438

US-10-141-761-438

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US-10-141-765-438

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STREET: 9410 Key West Avenue
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US-10-140-805-438
US-10-142-885-438
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US-10-142-426-438
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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STRANDEDNESS: double
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\begin{matrix} \mathsf{w} \, \mathsf{u} 
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Sequence 27, Appl
Sequence 3719, Ap
Sequence 206, App
Sequence 626, App
Sequence 438, App
Sequence 438, App
Sequence 40693, Ap
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213202,
46149, A
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148124,
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Sequence 254818,
Sequence 254819,
Sequence 254820,
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                                                                                                                                                                                                                               June 13, 2002, 12:42:33; Search time 279.06 Seconds
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(gn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

(gn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-673-476-626

US-10-027-632-5967

US-10-027-632-5967

US-09-789-1189-1128

US-09-789-1189-1128

US-09-789-1189-1128

US-09-673-476-671

US-10-027-622-13202

US-09-673-476-99

US-10-027-632-364116

US-10-027-632-2548116

US-10-027-632-2548116

US-10-027-632-2548116

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Listing first 45 summaries
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Result

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;	Qy 1141 CGTGGAAACTC3 	Qy 1201 AATCGACTACCC	1201	Qy 1261 CAAAAATATG 	Oy 1321 TGGAACTTACTE 	1381	1381	Qy 1441 CATGATGAAAAC              Db 1441 CATGATGAAAAC	Qy 1501 TCAGGCTGGTA/	1501	Qy 1561 GACCTCTCAATT 	Qy 1621 GGCTGTATGGAC               Db 1621 GGCTGTATGGAC	1691	1681	Oy 1741 TTGGAATATACC	1801	1801	Qy 1861 ATCAGATAGTTC 			OY 1981 TCCTCAACCAGG Db 1981 TCCTCAACCAGG	RESULT 2 US-10-121-120-27/c ; Sequence 27, Applice	; GENERAL INFORMATION; ; APPLICANT: Bergeror ; APPLICANT: Ouellet ; APPLICANT: Ooy, PE	; TITLE OF INVENTION ; TITLE OF INVENTION ; TITLE OF INVENTION
1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 60	TGCCCAAGCTAATGATATCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA		121 TCGCTTCTTCGACCACAGGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGAA 180 121 TCGCTTCTTCGACCACGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGAA 180	181 TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC 240	TTACTTTTCAACTTCGACCACCAGACTATTCTCGTAAGGCTCAGGAAGCTTGGTT	241 TTACTITICAACTICGACTICCGACCAGACTATITCTCGTAAGGCTCAGGAAGCTIGGTT 300	301 AGCGATTCAGTTAGAACAAAAGCAACCAAGCAAGAATCTTGACCTACTATATAAATAA	4 4	AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG		481 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCGAAACTTGGTCTT 540 		541 ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC 600	601 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 660	661 TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTAC 720	661 TAATTACCTCAAGGAAGTCATCAAGTTGAAGAAGAAGAGGCTATAACCTACTCAC 720	721 AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT 780 	781 TTACAATACAGACGAATACCTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 840 111111111111111111111111111111111111	TGTTGATGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCCACGCCATCAGTAAAA		901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAACAACCGCGACTGGGGATCAATGAA 960 	961 ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT 1020 	1021 CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG 1080 	1081 GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC 1140
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Primers
to Rapidly Detect and Identify Common Bacterial
Pathogens and Antibiotic Resistance Genes from Clinical
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ette, Marc
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APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
                                                                                                                                                                                                                                                                                                                                                                                                                293 tgatcgccacggaggacgttcgctttaccgaacattcgggtatcgatgccaaagcgctga 352
                                                                                                                                                                                                                                                                                                                                                  233 gtaaggaaaatcgtgtatacacctcttataatgaactttcacccaacattgtcaatgcat 292
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                                                                                                                                                                                                                                                                                                                                                                                   102 TCGTTTCTATCGAAGACCATCGCTTCTTCGACCACGGGGGATTGATACCATCCGTATCC
                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                     Length 2370;
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                                                                                                                                                                                                                                                                                   0; Mismatches 283;
                                                                                                                                                                                                                                                     Score 59.2; DB 5;
Pred. No. 2.2e-06;
                                                                                CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 3719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 206, Application US/09673476 GENERAL INFORMATION:
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                                                                                                                                                                                    ORGANISM: B.fragilis
US-09-540-209B-3719
                                                                                                                                                                                                                                                                  Similarity
        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   Matches 261;
                                                                                                                                                                      TYPE: DNA
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Best Local 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAATCTGCAAA---GCAATTCCCT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 TTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTTAGCGATTCAGTTAGAACA 318
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                                                                                                                                                                                                                                                                                                                  12;
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   Specimens for Routine Diagnosis in Micro
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les 333;
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                                                                                                                                                                                                                                                                                  Score 117.2;
Pred. No. 1.5e
0; Mismatches
FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/10/121,120
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/452,599
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-121-120-27
                                                                                                                                                                                                                                                                                  Query Match 5.9%;
Best Local Similarity 50.3%;
Matches 349; Conservative
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US-09-540-209B-3719
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                                                                                                                                                                                  LENGTH: 9100
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APPLICANT: COLE, STEWART
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: GORDON, STEPHEN
APPLICANT: GLIADULT, ALAIN
TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GRNOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: MYCOBACTERIA.
TITLE OF INVENTION: MYCOBACTERIA.
FILE REFERENCE: 05394.0011-00000
                                                                               353 tacgigotgiggtaaagcgiggattgotgatgcagaaaaatgcaggiggaggcagtacac 412
                                                                                                                                                                                                                                                        413 tttcacaacagctcgccaagcaattgtttacggacgaagttgccagaaatacgctgcagc 472
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aggaagaaattttgagtatgtatctcaataaatttgacttcctgaataatgcagtaggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                gcctgtttcagaagccgatagagtgggtgattgccgtaaaaactggaacgttattatacaa
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                                                                                                                                                                        TCACCCAACAGTTGATTAA----GTTGACTTACTTTTCAACTTCGACTTCCGACCAGA
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Sequence 438, Application US/09673476

GENERAL INFORMATION:
APPLICANT: COLE, STEWARY
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BULLAULY, ALAIN
TITLE OF INVENTION: AMETHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
FILE REFERENCE: 03394.0011-00000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/1899/00740
PRIOR APPLICATION NUMBER: PCT/1899/00740
                                                                                                                                                                                    386 GGAATGCAGACAGCAGCTCAAAACTACTATGGTAAAGACCTCAATAATTTAAGTTTACCT 445
                                                                                                                                                                                                                                    86 ggcgtgcaggacgcggcgaaacgtacttcggcatcaacgcgtccgacctgaattggcag 145
                                                                               326 ACCAAGCAAGAAATCTTGACCTACTATAAATAAGGTCTACATGTCTAATGGGAACTAT 385
                                                                                                                                                                                                                                                                                      446 CAGTTAGCCTTGCTGGCTGGAATGCCTCAGGCACCAAACCAATATGACCCCTATTCACAT 505
                                                                                                                                                                                                                                                                                                                      341 TIGACCTACTATATAAATAAGGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 GCTCAAAACTACTATGGTAAAGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTG 460
                                                                                                            6 aagettegegagateeggatggeaeteaegetggacaaagaeetteaeaaatetgaaate 65
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       Pred. No. 0.00013;
0; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
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; OTHER INFORMATION: a, t, c or g
US-09-673-476-438
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       52.68;
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SEQ ID NO 438
LENGTH: 223
       Best Local Similarity 52.6
Matches 113; Conservative
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GENERAL INFORMATION:
APPLICANT: COLE, STEWART
APPLICANT: COLE, STEWART
APPLICANT: GOLE, STEWART
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: GORDON, STEWHEN
APPLICANT: BULLAULY, ALAIN
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: MYCOBACTERIA.
TITLE OF INVENTION: MYCOBACTERIA.
TITLE OF INVENTION: WHORER: US/09/673,476
CURRENT APPLICATION NUMBER: PCT/1B99/00740
PRIOR FILING DATE: 1998-04-16
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN VUMBER: 202-416
NUMBER OF SEQ ID NOS: 743
SEQ ID NO 626
LENGTH: 363
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CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
FRIOR APPLICATION NUMBER: PCT/IB99/00740
PRIOR FILING DATE: 1999-04-16
PRIOR PELING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PatentIn Ver. 2.2
SEQ ID NO 206
LENGTH: 428
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; ORGANISM: Mycobacterium tuberculosis
US-09-673-476-626
                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                              TYPE: DNA
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392 AAAAGCAAGTGGGAAAAAAAAACACAAAAACAAAAATGAAAATGAGAGCTGAATTTTTAACGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1228, Application US/09789189
; Sequence 1228, Application US/09789189
; GENERAL INFORMATION:
; APPLICANT: Celias, Jean-Michel
; FILE REFRENCE: 25436/1720
; CURRENT APPLICATION NUMBER: US/09/789,189
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/183452
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 2005
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)._(242)
; OTHER INFORMATION: "n" at position 33 refers to any of G, A,
US-09-789-189-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 GAACTATGGAATGCAGACAGCACCTCAAAACTACTATGGTAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                  PRIOR PEDICATION NUMBER: US 60/185,218
PRIOR PELICATION NUMBER: US 60/167,318
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PELICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38;
Pred. No.
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(430)
; OTHER INFORMATION: n = A,T,C or
US-10-027-632-40693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%;
Best Local Similarity 60.8%;
Matches 62; Conservative
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LOCATION: (1)..(242)
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                SEQ ID NO 40693
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                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                        FILE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,28
PRIOR APPLICATION NUMBER: US 60/165,218
PRIOR APPLICATION NUMBER: US 60/165,368
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRASERD for Windows Version 4.0
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             DAPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-012,8,606

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: US 60/198,676
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                                                                                       461 GCTGGAATGCCTCAGGCACCAAACCAATATGACCCCTA 498
                                                                                                                                       186 gccggcatggtgcaatcnaccagcacgctcaacccgta 223
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                                                                                                                                                                                                                                                                   Sequence 5967, Application US/10027632 GENERAL INFORMATION:
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Best Local Similarity 55.1%
Matches 76; Conservative
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US-09-673-476-671/C
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LENGTH: 2409
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                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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GENERAL INFORMATION:
FOR TIME OF INVENTION:
FOR INVENTION:
FRIOR FILING DATE:
FOR INVENTION:
FRIOR PRICE APPLICATION NUMBER:
FOR INVENTION NUMBER:
FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   889 aagccaattgatgatttttacgttttgtcaactactgtctcagtgctatggtaaagtcc 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        829 ggagatgaagttggttgtatccttgcctattttatatttcaagaatacaaaaacgttgga 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746 GTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGACGAATACGTTGCC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.2;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                   Sequence 46474, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       866 ATTGCCCAGCTAGGAGCACGCCATCA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Schizosaccharomyces pombe US-60-360-039-46474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%;
Best Local Similarity 53.4%;
Matches 78; Conservative (
152 tataatataaactaac 167
                                                                                                                                                                                                                                                                              Chen, Xianfeng
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US-10-027-632-213202
                                                                                                                                   US-60-360-039-46474
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LENGTH: 679
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LENGTH: 1611
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Sequence 46149, Application US/60360039
Sequence 46149, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Staven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
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GENERAL INFORMATION:
APPLICANT: COLE, STEWART
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BILAULT, ALAIN
APPLICANT: BILAULT, ALAIN
APPLICANT: BILAULT, ALAIN
APPLICANT: BILAULT, REANING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
                                                                                                                                                                                                                                                       508 AAGAGAAATACAGATCAACACATACAATCACTATAAAATTTATTAAAAATTAAGAAGTT 449
                                                                                                                                                                                                                                                                                                                                    GCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCATTGTTGATGTTTCTAACGGTAAA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733 TGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGA 792
                                                                                                                                                      568 AAACTAAGAAAATAAGAATCAGATTTTAAAATATGTTAGGTTGAAATCCAACTAAAAACA 509
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  Length 679;
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Pred. No. 5.2;
0; Mismatches 74;
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Score 36.6; Di
Pred. No. 3.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-10(52052)A
CURRENT PAPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Saccharomyces cerevisiae US-60-360-039-46149
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Query Match 1.8%;
Best Local Similarity 49.2%;
Matches 96; Conservative
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Best Local Similarity 52.33
Matches 81; Conservative
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1892 ACCACTCCAAGCACAAATAATAGTACGACTACCAATCCTAACAATAATACGCAACAATCA 1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                        360 CCCCCTCCAGAGGATAATACTCCCTCTAGAAGATAATACTCCTCCTCCAGAAGATAAT 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 CCCTCGGACAAGATCGCCAACACGATGAAGCTGGCGATCGTCTCGATTGAAGATAAGCGG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 CAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGC 124
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                                                                                                                                                                                                                                                                                                                     1.8%; Score 36; DB 6; Length 689; 51.2%; Pred. No. 4.8;
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Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
    ; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148124
; LENGTH: 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mycobacterium tuberculosis US-09-673-476-99
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Best Local Similarity 51.6%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                     Query Match 1.8°
Best Local Similarity 51.2°
Matches 84; Conservative
                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-148124
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: US 60/185,218
FRIOR FILING DATE: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 ATGGTCGACGCGAAGGGCAACACGATCGCGTGGCTGNACTCGCAGCGCCGGTTCGAGGTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 CAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CCCTCGGACAAGATCGCCAACACGATGAAGCTGGCGATCGTCTCGATTGAAGATAAGCGG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 36.4; DB 5;
Best Local Similarity 51.6%; Pred. No. 3.2;
Matches 82; Conservative 0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTG 163
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FILE REFERENCE: 05394 0011-000000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/IB99/00740
PRIOR PILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
NUMBER: OF SEQ ID NOS: 743
SEQ ID NO 671
                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LOCATION: (468); OTHER INFORMATION: a, t, c or g
US-09-673-476-671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c or g
                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: a, t, c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (247)
OTHER INFORMATION: a, t, c
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OTHER INFORMATION: a, t, c
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OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                FEATURE: NAME/KEY: modified_base
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PI CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI
STEVEN C BARASH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10711;
                    pneumoniae and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 10711
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Fred. No. 0;
Mismatches
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. 2056 c 2412 g 296:
Polynucleotide of Streptococcus | BD003825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strandedness: Double;
                                                  BD003825.1 GI:18631786
JP 2001501833-A/145.
unidentified.
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Best Local Similarity 100.0%;
Matches 1999; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Topology:
                                                                                                        unidentified
unclassified
                                                                                                                                                                                                                                                                                                                                                                        PI MICHA
PC C12N1
PC C12N1
PC C12N1
CC C12N5
CC Stran
CC TOPOL
FT Key
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us-08-961-083-1.oli15.rge

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Strepcoccus, 1 (bases 1 to 11334)

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Strettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., DodSon, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angluoli, S., Dickinson, T., Hckey, E.K., Holt, J.E., Loftus, B.J., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M. Complete genome sequence of a virulent isolate of Streptococcus pneumoniae

AL Science, 293 (5529), 498-506 (2001)

El Gases I to 11334)

El Gases I to 11334)

Ettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Umayam, L.A., White, O. Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angluoli, S., Gesuwan, P., Hickey, E.K., Holt, I.E., Loftus, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M. Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M. Direct Submission
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Streptococcus pneumoniae TIGR4.
Streptococcus pneumoniae TIGR4
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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8028
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                                                                                                                                                                                                  GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT 1680
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                                                                                                                                                                                                                                                                                                                                             TTGGAATATACCAGAGGGGTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG
                                                                                  GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
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                                                                                                                AE007349 11334 bp
Streptococcus pneumoniae TIGR4
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GSSLFRRGYRTERGGAPIKENMASALIQLSNWYDNFBLEDIDMCGDIDARWVEIAKNA
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CHPEKNEYPEY DVESEVNSIEK PRETRIMANDAGPGTDATIOALLPHLDKGDTLIDGGN
CHPEKNEYPES TO TETER SCENGALEG PSIMPGGOKEA YELVADVLEEIS
AKAPEDGCKPCYTY IGEDGAGHYVKMYHNGIES GENGALEG SENDHAGGGELDSYLLIETADILSRKDDEGQDG PIVDYILDAAGNKGTGKWTSGSSLDL
GVPLSITTES VFARYISTYKEERVHASKVLPKFAAFNFEGDKAELIEKIRQALYFSKI
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YFGAHTYQRKDKEGTFHYSWYDEK"
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complement(2270. 2866)

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COMPLEMENT (2270 . . 2866)
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Submitted (29-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
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                                                                       FEATURES
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TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCATC 1860
                                                                                           TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTAA
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/product="choline binding protein C"
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/translation="MKLLKKMMQVALAVFFEGLLATNTVFANTTGGREVDKDNRKYYV
KDAPKAIYMHKIDGKTYYFGDIGEMVVGWQYLEIPGTGYRDNLFDNQPVNEIGLQEKW
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TDWQKVNGKWYYFGSSGSMATGWKYNGKWYYLDNKNGDMKTGWQYE
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/gene="Sp0378"

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/gene="Sp0378"

/codon_start=1

/transl_table=11

/product="choline binding pr

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/db_xref="GI:14971847"
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Ferroni, A. and Berche, P.
Alterations to penicillin-binding proteins 1A, 2B and 2X amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23F from the nasopharyngeal flora of children J. Med. Microbiol. 50 (9), 828-832 (2001)
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 TICTACGIGGAACICACCIGCICCACAACAACCCCCAICAACIGAAAGIICAAGCICAIC 256
                                 TACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGAA
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Ferroni,A. and Berche,P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospital
Necker-Enfants-Walades, 149 rue de Sevres, Paris
Location/Qualifiers
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/organism="Streptococcus pneumoniae"
/serctype="23F"
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X67873.1 GI:47419
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               TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA
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                                                                                                               CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTACGCTGCCTTTGCAAATGG
                                                                                                                                              TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA
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                                                CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAGG
                                                                               AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAAACCGAATCAGA
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DEFINITION ACCESSION VERSION

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/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
/protein_id="CAA48073.1"
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/db_xref="%II:47420"
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pénicillin-binding protein la; ponA gene.
Streptococcus pneumoniae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group;
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Hakenbeck, R.
Direct Submission
Submitted (24-JUL-1992) R. Hakenbeck, Max-Planck
Genetik, Ihnestr. 73, 1000 Berlin 33, FRG
2 (bases 1 to 2157)
Martin, C., Sibold, C. and Hakenbeck, R.
Relatedness of penicillin-binding protein 1a ger
clones of penicillin-resistant Streptococcus pne
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/strain="45607"
/db_xref="taxon:1313"
/clone="pcMK1-pcMK16"
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EMBO J. 11 (11), 3831-3836 (1992)
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/transl_table=11
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AF210746 2160 bp DNA linear BCT 17-SEP-2001 Streptococcus pneumoniae isolate SP 1513 penicillin-binding protein 1A (pbpla) gene, complete cds. AF210746 AF210746.1 GI:6563338
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaes;
Streptococcus.

(bases 1 to 2160)
Ferroni,A. and Berohe,P.
Ferroni,A. and Berohe,P.
Ferroni,A. and Berohe,P.
Ferroni,A. benicillin-binding proteins 1A, 2B and 2X amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23F from the nasopharyngeal flora of children
J. Med. Microbiol. 50 (9), 828-832 (2001)
21432820
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Ferroni,A. and Berche,P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospital
Necker-Enfants-Malades, 149 rue de Sevres, Paris 75015, France
Location/Qualifiers
1. 2160
                                                                                                                         1779 GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT
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/serotype="23F"
/isolate="SP 1513"
/db_xref="taxon:1313"
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                                                      /transl_table=11
                                               /codon_start=1
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/product="penicillin-binding protein la"
/brotein_id="CAA48072.1"
/db_xref="G1:47418"
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Submitted (24-JUL-1992) R. Hakenbeck, Max-Planck Inst.
Genetik, Innestr. 73, 1000 Berlin 33, FRG
( Lases 1 to 2157)
Martin,C., Sibold,C. and Hakenbeck,R.
Relatedness of penicillin-binding protein la genes from
clones of penicillin-resistant Streptococcus pneumoniae
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Bergeron, M.G., Boissinot, M., Huletsky, A., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to for detection of microorganisms patent: WO 0123604-A 2048 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA) DNA В ψ. 2160 bp Di from Patent WO0123604. Location/Qualifiers
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SKLVATTSSKIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGID
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GLATUHKPPPIQIVQVDYPORSRAFTYPAYFRAZ
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SMPLEYIREYGYEIRAGAFPQIPYLNVIKEHLLGGKTR
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Martin,C., Briese,T. and Hakenbeck,R.
Nucleotide sequences of genes encoding penicillin-binding proteins from Streptococcus pneumoniae and Streptococcus oralis with high homology to Escherichia coli penicillin-binding proteins 1A and 1B 9.2325042
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/gene="ponA"
/function="unknown"
/note="ORF"
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/trans1_table=11
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ilarity 99.4%;
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Best Local Similarity
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IVHDEPYNYPGTNTPVYNWDRGYFGNITLQYALQQSRNVPAVETLMKVGLNRAKTFLN
GGGIDYPSITYSNALSSNTYEBDKKYGASSEKMAARARARARANGTYYKPR
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kraipmknfhphqiqhmeqvlaqqgicfvllhfssqqetyllpafdlirfyhqdkgqk
Smpleyireygyeikagafpqipylnvikehllggktr"
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VKYAYPRYEHKGQLRDYQQFLLENTTSSYLFYDEENETKLAYFYQKMKNQEDYFIKRL
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MIARKMAPGLERSFAPEEWNWISDRLIQENFPAAKKWERELELDIMGCDIDARWYEI
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VFAPLKTWSKFILTSDEAFESKYGSQARKKKLYNGTLKVUDYFGQRYKROEVK
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AKCVKSKLHNEPSVQAISKKAVVKKLQKHYARPEGVPLMENGPEFKIEVSILKDVATV
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4329. 5501
/gene="spr0333"
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/note="Putative"
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TRILGAFLENLQSNSLQGGSALTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEÖK
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Hoskins, J.A., Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, S., DeHoff, B.S., Estrem, S., Fritz, L., Fu, D. J., Fuller, W., Geringer, C., Gilmour, R., Glass, J.S., Hann, A., Khoja, H., Kraft, A., Ladace, R., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., McHenney, M., McLeaster, K., Mundy, C., Nicas, T.I., Norris, F.H., O'Gara, M., Peery, R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R., Jr., Skatrud, P.L.
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Submitted (27-JUL-2001) Infectious Diseases Research, Eli Lilly and
Company, Lilly Research Labs, Indianapolis, IN 46285-0438, USA
Location/Qualifiers
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1 (bases 1 to 10313)
Hoskins, Ja., Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, S., Benoff, B.S., Estrem, S., Fritz, L., Fu, D.-J., Fuller, W., Geringer, C., Gilmour, R., Glass, J.S., Khoja, H., Kraft, A., LaGace, R., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., McHenney, M., McLeaster, K., Muddy, C., Nicas, T. I., Norris, F.H., O'Gara, M., Peery R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L.
AE008414 10313 bp DNA linear BCT 13-SE
Streptococcus pneumoniae R6 section 30 of 184 of the complete
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/EC_number="2.4.1.129"
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/protein_id="AAK99138.1"
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                                                                                                                                                                                                                                                            /db_xref="GI:15457891"
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8420. 9109
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/gene="spr0334"
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Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouel Plotard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes if for detection of microorganisms
Patent: WO 0123604-A 2060 05-APR-2001;
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Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)
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Asahi,Y.

Direct Submission
Submitted (27-AUG-1997) Yasuko Asahi, Teikyo University School
Medicine, Department of Clinical Pathology; 2-11-1 Kaga.

Itabashi-ku, Tokyo 173-8605, Japan
(E-mail:asahi@med.teikyo-u.ac.jp, Tel:81-3-3964-1211,
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/product="penicillin binding protein lA"
/protein_id="BAA32070.1"
/db_xref="G1:3395652"
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AB006874
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THE TRANSPAPQOPPSTESSSSSSSSSSSSSTSGSSTTPSTNNSTTTDPNNNTQOSNTTPDQON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 ATGTATATCCATAAAGTCGTCTTTAGTGATGGAGTGAAAAAGAGTTCTCTAATGTCGGA
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Best Local Similarity 99.5%;
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SEKMAAAYAAFANGGTYYKPWYIHKVVFSNGSQKEFSNVGYRAMKETTAYMYDDMKY
VLSYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAV
WTGYSNRLTPLVGNGLTVAAKYYSSMATYLSEGSNPEDWNIPEGGLYRNGFRNGAR
STWSSPAPQQPPSTESSSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQN
ONPQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcaceae;
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             TCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGTCGCTGCCAAAGTTTACCGC
                                                                                                    CTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCGTTCTACGTGGAACTCACCT
                                                                                                                                                                                                                                                                           TCTATGATGACCTACCTGTCTGAAGGAAGCAATCCAGAAGATTGGAATATACCAGAGGGG
Direct Submission
Submitted (27-AUG-1997) Yasuko Asahi, Teikyo University
Medicine, Department of Clinical Pathology; 2-11-1 Kaga,
Itabashi-ku, Tokyo 173-8605, Japan
(E-mall:asahi@med.telkyo-u.ac.jp, Tel:81-3-3964-1211,
Fax:81-3-3963-6023)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Streptococcus pneumoniae
Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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/protein_id="BAA32064.1"
/db_xref="G1:3395640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pbpla; penicillin binding protein 1A.
Streptococcus pneumoniae (isolate:#1/H23) DNA.
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/transl_table=11
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<1. .>1195
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Asahi,Y.
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FEATURES
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SPPONA6 1826 bp DNA linear BCT 11-MAY-1995
S.pneumoniae (8250) ponA gene for penicillin-binding protein la.
X67871
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pneumoniae isolated in
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                                                                 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA
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                                                      ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAAGCAGTCAATAC
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Submitted (24-JUL-1992) R. Hakenbeck, Max-Planck Inst.
Genetik, Ihnestr. 73, 1000 Berlin 33, FRG
2 (bases 1 to 1926)
Martin, C., Sibold, C. and Hakenbeck, R.
Relatedness of penicillin-binding protein la genes from clones of penicillin-resistant Streptococcus pneumoniae
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Protein_id="CAA48071.1"
/db_xref="GI:47416"
/db_xref="SPTREMBE:Q54951"
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Streptococcus pneumontae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridiu
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EMBO J. 11 (11), 3831-3836 (1992)
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/codon_start=1
/transl_table=11
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Hakenbeck, R.
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Masure,H. Robert, Pearce,B.J. and Tuomanen,E.
Bacterial exported proteins and acellular vaccines based thereon
Patent: US 5981229-A 3 09-NOV-1999;
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Pred. No. 0;
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Squence 3 from patent US 5981229,
AR084885
AR084885.1 GI:10011656
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224 c 182 g
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TILGAFLKNLQSISTGGGSTLTQOLIKITYFSTSTSDQTTSRKQDEAMLAIQLEQK
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DGSEKEPSNYGTRAMREAAAYMFRAMKKTVLTYGIGRGAXLPWLPQAGKTGTSNYTDE
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/product="pending lilin-binding protein lA"
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YSHPEAAQDRRNLVLSEMKNQGYISAEQYEKAXNTPITDGLQSLKSASNYPAYMDNYL
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DVSNGKVIJAGLGSRHQOSNOVSFGINQVYTRNRGAAKRYTIOTAPALEZDIYDSTAS
IVHDVPYNYPGTDPTELNWDKYYFGNITIOYALQQSRNVTAVFELIKKVGLDRAKTFLM
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LSEDNNPGDWTMPEGLYRSGEFVFKKGARSAWTAPAPQQAPTPESSSSTSESSTSQSS
                                                                                                                                                                                                                  linear BCT 17-SEP-2001 penicillin-binding protein
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Ferroni, A. and Berche, P.
Alterations to pericillin-binding proteins 1A, 2B and 2X
penicillin-resistant clinical isolates of Streptococcus p
serotype 23F from the nasopharyngeal flora of children
J. Med Microbiol. 50 (9), 828-832 (2001)
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group;
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497 c 419 q 559 t 1 ot)
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...prococcus pneumoniae isolate SP 1258 per
1A (pbpla) gene, partial cds.
AP210748
AF210748.1 GI:6563342
Strenfor-
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Ferroni, A. and Berche, P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospi
Necker-Enfants-Malades, 149 rue de Sevres, 1
Location/Qualifiers
1. 2154
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Matches 855; Conservative
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KEYWORDS
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GYTRKYAAAVWTGYSNRLTPLVGNGLTVAAKVYR"

87 215 c 198 g 229 t
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  essential for high-level penicillin
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resistance in Streptococcus pneumoniae
Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
98287565
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                                          2 (bases 1 to 930)
Smith, A.M.
Direct Submission
Submitted (06-FEB-1998) Microbiology,
Gauteng 2000, South Africa
Location/Qualifiers
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al Similarity 100.0%; Pred. No. 0;
671; Conservative 0; Mismatches
                                                                                                            1. .930
/organism="Streptococcus
                                                                                                                                  /strain="64429"
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                                                                                                                                                                /gene="ponA"
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Best Local S
Matches 671
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penicillin-binding protein 1A
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                     TAATTACCTCAAGGAAGTCATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC
                                                                                                             TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC
                                                                                                                                                       TTACTITICAACTICGACTICCGACCAGACTATITCTCGTAAGGCTCAGGAAGCTIGGTI
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Smith, A.M. and Klug
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AUTHORS
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Streptococcus pneumoniae strain 17619 penicillin-binding protein lA AF046237.1 GI:2911419
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Submitted (06-FEB-1998) Microbiology, SAIMR Hospital, Johannesburg,
Gauteng 2000, South Africa
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                        AACTGGGATAGGGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGA
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1 (bases 1 to 930)

1 (bases 1 to 810)

Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae
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/organism="Streptococcus pneumoniae"
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<1. .>930
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Smith, A.M.
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/product="penicillin-binding protein la"
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83 a 214 c 198 g 235 t
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Direct Submission
Submitted (06-FEB-1998) Microbiology, SAIMR Hospital, Johannesburg,
Gauteng 2000, South Africa
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Smith, A.M. and Klugman, K.P.
Alterations in PBP 1A essential for high-level penicillin
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Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
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Pred. No. 0;
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/organism="Streptococcus
/strain="7851"
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                            Huletsky, A.,
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Bergeron, M.G., Boissinot, M., Huletsky, P. Picard, F.J. and Roy, P. H.
Highly conserved genes and their use to detection of microorganisms
Patent: WO 0123604-A 2053 05-APR-2001;
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Sequence 2053 from Patent W00123604
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Pred. No. 0
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212 c 196 g
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Location/Qualifiers
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                                         Streptococcus pneumoniae
                    AX111320.1 GI:13927612
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Matches 670; Conservative
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                                       /product="penicillin-binding protein lA"
/protein_id="AAC24702.1"
/db_xref="GI:2911420"
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Description of the control of the control of the control of many of the control of microorganisms patent: WO 0123604-A 1017 05-APR-2001; Infection Diagnostic (T.D.I.) INC. (CA)
                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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 541 TACGCTGCCTTTGCAAATGGTGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTC
                                         745 TGTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGACGAATACGTTGC
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Sequence 1017 from Patent W00123604.
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/organism="Streptococcus
/strain="StrR-14"
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287 c 240 g
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Best Local Similarity 99.7
Matches 667; Conservative
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Pred. No. 0;
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/db_xref="taxon:1313"
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Bergeron,M.G., Boissinot,M.,
Picard,F.J. and Roy,P.H.
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99.7%;
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                                                      RESULT 2
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Streptococcus pneumoniae strain 56739 penicillin-binding protein lA (ponA) gene, partial cds.
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Submitted (06-FEB-1998) Microbiology, SAIMR Hospital, Johannesburg,
Gauteng 2000, South Africa
Location/Qualifiers
                                                                                                                             950 TCAACTATGAAACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCA 1009
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Smith, A.M. and Klugman, K.P.
Alterations in PBP 1A essential for high-level penicillin
resistance in Streptococcus pneumoniae
Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
98287565
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Streptococcus pneumoniae
Bacteria: Firmicutes; Bacillus/Clostridium group;
Streptococcus.
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/organism="Streptococcus pneumonjae"
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<1. .>930
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<1. .>930
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Smith, A.M.
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/transl_table=11
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/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
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TESDNKYRGASSERANAARAARANAFHNTHKVYFSDGSEKEFSNVGTRANKETT
AYMATEMMKTVLVVGIGRAYLDWLPQAGKTGTNYTDEEIEKYIKNTGYVAPDEMFV
GYTRKYAMAVWTGYTNRLTPVVGGGFTVAAKVYR"
87 a 213 c 201 g 229 t
                                                                                                                                                                                                                                                                            Streptococcus pneumoniae strain N94 penicillin-binding protein lA (PonA) gene, partial cds.
AF046236
AF046236.1 GI:2911417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (06-FEB-1998) Microbiology, SAIMR Hospital, Johannesburg,
Gauteng 2000, South Africa
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                           540
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Streptococcus.

The (Dases 1 to 930)
Smith, A.M. and Klugman, K.P.
Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae
Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
98287565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 551; DB
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .930
/organism="Streptococcus pn
/strain="N94"
/db_xref="taxon:1313"
<1. .>930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae. Streptococcus pneumoniae
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/note="PBP 1A"
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<1. .>930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 930)
Smith, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 651; Conservative
                                                                                                                                                                                         1405 TGCCATGAA 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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ORIGIN
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JOURNAL
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TITLE
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AUTHORS
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ATKOEILTYYINKYMSNGNYGGTSTLTQQLIKLTYFESTSTSDGT1SRKAQBAMLATQLEQK
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KEVIDQVEGTGYNLLTTGMDVYTVDQEGARHQANDIYNSDGYVSTPDDLQVASTVV
DVSNGKYINQLGARHQASNVSFGTNOAVETNRDWGSTWKRPITDYAPAIETGYVDSTAT
MVNDIPYNYPGTSTPVYNWDRAYFGNITLQYALQQSRNVPAVETLNKYGLDBRAKNFLN
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OGESERERSDAGGTRAMKETTAYMHTEMMKTVLSYGGRNAYLAHLDQAGKRGTSNYTDE
EIENIIKTSQFVAPDELFAGYTRK SMAYMTGYSNRLFPLVGNGLIYVAAKVSEMMY
LSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWSSPAPQQPPSTESSSSSSSSSSS
                                                     Streptococcaceae;
                                                                 Streptococcus.

1 (bases 1 to 2160)
Ferroni, A. and Barche, P.
Alterations to penicillin-binding proteins 1A, 2B and 2X amongst
penicillin-resistant clinical isolates of Streptococcus pneumoniae
serotype 23F from the nasopharyngeal flora of children
J. Med. Microbiol. 50 (9), 828-832 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1620 TTATGGAACTGGACGAAATGCCTATCTTGCTTGGCTCCCTCAGGCTGGTAAAACAGGAAC 1679
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                                                                                                                                                                                                                                                                                  ly, Hospital
Sevres, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATGGAACTGGACGAAATGCCTATCTTGCTTGGCTCCCTCAGGCTGGTAAAACAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1522 CTCTAACTATACAGACGAGGAATTGAAAACCACATCAAGACCTCTCAATTTGTAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1582 TGATGAACTATTTGCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTC
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                                                     group;
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505 c 405 g 558 t
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            Streptococcus pneumoniae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium
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Pred. No. 3e-234;
0; Mismatches 2
                                                                                                                                                                                                                       (bases 1 to 2160)
Ferroni, A. and Berche, P.
Direct Submission
Submitted (03-DEC-1999) Microbiology,
Necker-Enfants-Malades, 149 rue de Sev
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. 2160
/organism="Streptococcus pr./serotype="23f"
/isolate="SP 1465"
/db_xref="taxon:1313"
1. 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="pbpla"
1. .2160
/gene="pbpla"
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99.6%;
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21432820
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Best Local S
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                                  ORGANISM
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                             /codon_start=1
/transl_table=11
/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
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AYMMTEMMKTVLYGIGRGAYLDWLPQAGKTGTSNYTDBEIEKYIKNTGYVAPDEMFV
GYTRKYAMAWTGYSNRLTPLVGONGLTVAARVYR"
88 a 216 c 196 g 230 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1130 AACGTCCCAGCCGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCCAAGACTTTCCTA 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGGTCTAGGAATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACA 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
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                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                               Score 461; DB 1; I
Pred. No. 2.3e-248;
0; Mismatches 3;
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SP 1465 p
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                                                                                                                                                                                                                                                                                               23.18;
'gene="ponA"
                                                                                                                                                                                                                                                                                                                                   611; Conservative
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1582 TGATGAACTATTTGCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTC 1641
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TITLE
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PUBMED
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LOCUS
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SOURCE
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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*** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                    GTCTAGCTCAACCACTCCAAGCACAATAATAGTACGACTACCAATCCTAACAATAATAC 1941
                                                                                                                                                                     2040 GTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGACTACCAATCCTAACAATAATAC 2099
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Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.
Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.
Direct Submission
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                                                                                                                                                                                                                   Submitted (31-ocr-2000) Research Department, Glaxo Wellcome, Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a "vorking draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* Location/Qualifiers
                                                                                                    1980 FCCACAACCCCCATCAACTGAAAGTTCAAGCTCATCATCAGATAGTTCAACTTCACA
               CTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCGTTCTACGTGGAACTCACCTGC
                                 1920 CTACAGAAATGGAGAATTGGTATTTAAAAATGGTGCTCGTTCTACGTGGAGCTCACCTGC
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/serotype="19F"
/db_xref="taxon:1313"
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Pred. No. 2.9e-234;
0; Mismatches 2;
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Best Local Similarity 99.6%;
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MEDLINE
REFERENCE
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AF210752 2160 bp DNA linear BCT 17-SEP-2001 Streptococcus pneumoniae isolate BM 4200 penicillin-binding protein AF210752
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/db_xref="G1:6563351"
/tb_xref="G1:6563351"
/translation="MNKPITIRLIKYLSISFLSLVIAAIVLGGGVFFYYVSKAPSLSE
SKLVATTSSKIYDNIKQLIADLGSERKVNAQANDIPFDLVKAIVSIEDHRFFPHRGID
TIRILGAFLRNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQK
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1 (bases 1 to 2160)
Ferroni,A. and Berche,P.
Alterations to penicillin-binding proteins 1A, 2B and 2X amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae scrotype 23F from the nasopharyngeal flora of children
J. Med. Microbiol. 50 (9), 828-832 (2001)
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                       1642 TAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGTCGCTGCCAAAGTTTACCGCTC 1701
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Sevres, Paris 75015, France
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8028 TGATGAACTATTTGCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTC
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Ferroni, A. and Berche, P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, IN
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/isolate="BM 4200"
/db_xref="taxon:1313"
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YSHPEAAQDRRNIVLSEMKNGYISAEQYERAVNTPTTDGLGGSLKSASNYPAYMDNYL
KEVINGVEETGYNLLTTGMDVYTNVDGEAQKHLWDIYNTDEYVAYPDDELQVASTIV
DVSNGKVIAQLGARHQSSNVSFGINQAVETNBWGSPWKPAYBTLNKYGLNRAKTTV
IVHDEPVINPGTDTPVXWNDRGYFGNITLQYALQOSRNVPAYBTLNKYGLNRAKTFLN
GLGIDYPSLHYSTDTPVXWNDRGYFGNITLQYALQOSRNVPAYBTLNKYGLNRAKTFLN
GLGIDYPSLHYSTTARAISSNTTESDKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
BCSEKEFSNVGTRAMKETTAYMTDMMKTVLVYGIGRGAYLPPLVGDGLTVAAKVYRSNMTY
LSGGSNPEDMNTQQSYTRKYAMAYWTGYSNRLTPLVGDGLTVAAKVYRSNMTY
LSGGSNPEDMNTPQGSNTFRYRYAMAYWTGYSNRLTPLVGDGLTVAAKVYRSNMTY
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Pred. No. 5.4e-232;
0; Mismatches 12;
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA
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                                                                                              ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT
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Pred. No. 1.2e-211;
0; Mismatches 6;
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Bergeron, M.G., Boissinot, M., Huletsky, A., Picard, F.J. and Roy, P.H.

Highly conserved genes and their use to g for detection of microorganisms

Patent: WO 0123604 A 2047 05-APR-2001;

Infectio Diagnostic (1.D.I.) INC. (CA)

Location/Qualifiers

1. 2160

/organism="Streptococcus pneumor/strain="CS109"

/db_xref="taxon:1313"

/db_xref="taxon:1313"
                                                                                                                                                                                                                                                                                                                                                       Huletsky, A.,
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                                                                                                                                                                                                                        Sequence 2047 from Patent W00123604. AXIII314.1 GI:13927606
                                                                                                                                                           1179 CGTTCACGATGAGCCCTATAACTA 1202
                                                                                                                                             CGTTCACGATGAGCCCTATAACTA 1044
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99.1%;
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les 696; Conservative
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ORIGIN
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AUTHORS
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GLGIDYPSMHYANAISSNTTESNKKYGASSEKMÄÄAVAAFANGGIYHKPMYINKIVFS
BOESKERSDAGTRAMKETYAYMTEMKTYLLYFGTGRAYLYHLDQAGKTGTSNYTDE
ELEKYIKHTGYVAPDBENGYTRKYAMAVWTGYSNRLTPIIGDGFLYAGKYTSSMITY
LSEDDQPGDWTMPDGLYRNGEFVFKNGARSTWSSPAPQQPFSTESSSSSSSSSTSQSN
STPFSTNASTTYNPNNNTQQSNTTPDQQNQNPQPAQP

//gene="pbpla"
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IVHDVPYNYPGTDTPLYNWDHVYFGNITIQYALQQSRNVTAVETLNKVGLDRAKTFLN
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Pred. No. 1.2e-211;
0; Mismatches 6;
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S.pneumoniae CS111 pbpla gene
249095 1 GI:984230
                                                                                                                   /note="active site"
495 c 398 g
                                                                                                                                                                                             19.8%;
99.1%;
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Best Local Similarity 99.1
Matches 696; Conservative
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/evidence=experimental
/product="penicillin-binding protein la"
/product="penicillin-binding protein la"
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/db_xref="G1:984229"
/db_xref="SFYERBHL:057114"
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/translation="MNKPTILRLIXENTYSELSIEFLSLVIAAIVLGGGVFFYYVSKAPSLSE
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TIRILGAFLRNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRRAQEAMLAIQLEQK
ATROEILTYYINKVASNGNYGMQATAANYSKGRAVNPTTDGTQSLKASSNYPAYMDNYL
KSVINQVEEFGYNLLTTGMDVYTNVDQEAQKHLMDIYNSDQYVSYPDDDLQVASTVV
DVSNGKVIAQVEEFGYNLLTTGMDVYTNVDQEAQKHLMDIYNSDQYVSYPDDDLQVASTVV
                                                                                                                                                                                                                                                                                                                                                                              S.pneumoniae CS109 pbpla gene for penicillin-binding protein la. 249094.1 GI:98428
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/organism="Streptococcus pneumoniae"
/strain="CS109 (cephalosporin-resistant clinical isolate)"
/db_xref="taxon:1313"
13. .2172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="peptidoglycan transglycosylase-transpeptidase"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2172)
Coffey, T.J., Daniels, M., McDougal, L.K., Dowson, C.G., Tenover, F. and Spratt, B.G.
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GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 420
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                                                                                                                     AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCCAAGACCGCCGAAACTTGGTCTT
                                                                                                                                     Direct Submission
Submitted (21-APR-1995) Spratt B. G., University of Sus
of Biology, Falmer, Brighton, East Sussex, UK, BNI 9QG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                PBP 1A gene; penicillin-binding protein la
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13. .2172
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Spratt, B.G.
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LOCUS
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AUTHORS
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REFERENCE
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JOURNAL
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SOURCE
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Streptococcus pneumoniae partial pbpla gene for penicillin binding protein la, strain 960036.
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AJ403975.1 GI:12055852
Appla gene; penicillin binding protein 1A.
Streptococcus pneumoniae.
Streptococcus pneumoniae.
Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 489)
Overweg, K., Bogaert, D., Sluijter, M., de Groot, R. and Hermans, P.W.M.
Molecular characterization of Streptococcus pneumoniae
penicillia-resistance in the Netherlands
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="peptidoglycan transglycosylase-transpeptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (25-MAY-2000) Hermans P.W.M., Laboratory of Pediatrics,
Erasmus University Rotterdam, PO Box 1738, 3000 DR Rotterdam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC 600
    351 TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAATTGAC 410
                                                               411 TTACTTTTCAACCTCGACTTCCGACCAGACTATTCTCGTAAGGCTCAGGAAGCTTGGTT
                                                                                                                                                  GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                        601 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA
                                                                                                                            481 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACGGCGGAAACTTGGTCTT
                                             241 TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .489 //organism="Streptococcus pneumoniae" /strain="960036" //db_xref="taxon:1313"
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/gene="pbpla"
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/gene="pbp1a"
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Streptococcus pneumoniae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                               Direct Submission Spratt B. G., University of Sussex, School Submitted (21-APR-1995) Spratt B. G., University of Sussex, School Submitted (21-APR-1995) Spratt B. G., University of Sussex, School of Biology, Falmer, Brighton, East Sussex, UK, BNI 90G (2 (bases 1 to 2172) Coffeyyr.J., Daniels,M., McDougal,L.K., Dowson,C.G., Tenover,F.C. Genetic analysis of clinical isolates of Streptococcus pneumoniae with high-level resistance to expanded-spectrum cephalosporins Antimicrob. Agents Chemother. 39 (6), 1306-1313 (1995)
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Pred. No. 1.2e-211;
0; Mismatches 6; Indels
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/gene="pbp1a"
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13. .2172
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                /organism="Streptococcus pneumoniae"
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Best Local Similarity 99.6%; Pred. No. 1.4e-206;
Matches 487; Conservative 0; Mismatches 2;
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WGSTWKPITDYAAPALEYGVYDSTATIVHDEPYNYPGINTPVYNWDRGYFGNITLQYAL
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Streptococcus pneumoniae partial pbpla gene for penicillin binding
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Overweg.K., Bogaert,D., Sluijter,M., de Groot,R. and Hermans,P.W.M.
Molecular characterization of Streptococcus pneumoniae
penicillin-resistance in the Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-MAY-2000) Hermans P.W.M., Laboratory of Pediatrics, Erasmus University Rotterdam, PO Box 1738, 3000 DR Rotterdam,
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Pred. No. 1.4e-206;
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isolated
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/protein_id="CAA48068.1"
/db_xref="G1:47406"
                                                          Direct Submission
Submitted (24-JuL-1992) R. Hakenbeck, Max-Plan
Genetik, Ihnestr. 73, 1000 Berlin 33, FRG
C (bases 1 to 2157)
Martin,C., Sibold,C. and Hakenbeck,R.
Relatedness of penicillin-binding protein lacelones of penicillin-resistant Streptococcus South Africa and Spain
                                                                                                                                                                                                                                                                                                                                  pneumoniae"
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Pred. No. 1.3e-167;
0; Mismatches 7;
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93010977
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99.0%;
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                1 (bases 1 to 2157)
Hakenbeck, R.
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Best Local Similarity 99.0°
Matches 668; Conservative
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/db_xxef="SPTREMBL:054947"
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SKLVATYSSKIYDNKADLIADLGSBRRVNAQABDIPPDLVKATVSIEDHRFFDHRGID
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ATKQETLTYYINKYNSNGNYGMQTAAQNYGKDLNNISLPQLAGMPQAPQYPQYP
YSHPEAAQDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLGSLKSASNYPAYMDNIL
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for penicillin-binding protein la.
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DVSNGKVIAQLGARHQASNVSFGTNQAVETNRDWGSAMKPITDYAPAIEYGVYDSTAT
MVNDIPYNYPGTSTPVYNWDRAYFGNITLQYALQQSRNVTAVETLNKVGLDRAKTFLN
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Submitted (24-JUL-1992) R. Hakenbeck, Max-Planck Inst. fuer Molek.
Genetik, Thnestr. 73, 1000 Berlin 33, FRG
2 (bases 1 to 2157)
Martin,C., Sibold,C. and Hakenbeck,R.
                                                                                                                                                                                                                     ATCTGAAATGAAAAACAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC 600
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/db_xref="GI:47408"
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penicillin-binding protein la; ponA gene.
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/organism="Streptococcus |
/strain="681"
/db_xref="taxon:1313"
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EMBO J. 11 (11), 3831-3836 (1992)
93010977
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/transl_table=11
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/gene="ponA"
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Molek

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                               Max-Planck
        Hakenbeck, R.

Direct Submission

Submitted (24-JUL-1992) R. Hakenbeck, Max-Planck
Genelik, Ihnestr. 73, 1000 Berlin 33, FRG

2 (bases 1 to 2157)

Martin, C., Sibold, C. and Hakenbeck, R.
Relatedness of penicillin-binding protein la gen
clones of penicillin-resistant Streptococcus pne
South Africa and Spain
EMBO J. 11 (11), 3831-3836 (1992)
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Pred. No. 1.3e-167;
0; Mismatches 7;
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1. .>2157
/gene="pona"
/gene="pona"
/codon_start=1
/transl_table=11
/product="penicillin-binding pr
/protein_id="caa448067.1"
                                                                                                                                        1. .2157
/organism="Streptococcus pr
/strain="670"
/db_xref="taxon:1313"
/clone="pcMK1-pcMK16"
                                                                                                                            Location/Qualifiers
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99.0%;
(bases 1 to 2157)
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Best Local Similarity
Matches 668; Conserv
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                                                                                                                                        source
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ORIGIN
                                                              AUTHORS
TITLE
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                     TITLE
JOURNAL
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FEATURES
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            AUTHORS
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DGSKKEFSDVGTRAMKETTAYMMTEMMKTVLAYGTGRGAYLPWLAQRGKTGTSNYTDD
EIEKHIKKSTYVAPDEMFVGYTRKYSMAVWTGYSNRLTPIVGDGFLYAAKVYRSMITY
LSEDTHPEDTMPDGLFRNGFFVFKNGARSTWNSPAPQQPPSTESSSSSSSSSSSSSS
STTPSTNNSTTTPOGNONPOPAQP"

494 c 405 g 562 t
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X67867.1 GI:47409
penicillin-binding protein la; ponA gene.
Streptococcus pneumoniae.
Streptococcus pneumoniae.
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
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for penicillin-binding
                                                                                                                  Indels
                                                                                             Score 318; DB 1; Pred. No. 1.3e-167; 0; Mismatches 7;
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99.0%;
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S.pneumo
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Best Local S:
Matches 668
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DEFINITION
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SOURCE
ORGANISM
                                                    BASE COUNT
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DGSKKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRGAYLPWLPQAGKTGTSNYTDE
EVENIIKNTGYVAPDEMFVGYTRKYSNAVWTGYSNRLTPIVGDGFLVAAKVYRSMITY
LIEDTHPEDWTMPDGLFFNGEFVFKNGARPIWTEPSTQQSSTAESSSSSSSSSTSGSS
STTESTNNSTTANNNTTPDQQNQNPQPAQP"

494 c 403 g 564 L
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                    Score 318; DB 1; I
Pred. No. 1.3e-167;
0; Mismatches 7;
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99.0%;
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/product="pen.iolin-binding protein la"
/protein_id="CAA48069.1"
/db_xref="GI="47412"
/db_xref="SPREMBL:054949"
/db_xref="SPREMBL:054949"
/db_xref="SPREMBL:054949"
/translation="MNRPTILRLIKYLSISFLSLVIAAIVLGGGVFFYYVSKAPSLSE
SKLVATTSSKIYDNKNQLIADLGSRRRWAQANDIPPDLVKALVSISDHRFROID
SIRILGAFLRNLQSNSLGGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAMLAIOLEGK
ATKQEILTYYINKVYMSNGNYGMONTRAQNYTSTSDQTISRKAQEAMLAIOLEGK
ATKQEILTYYINKVYMSNGNYGMOTRAQNYTSTDGLOSLALAGAPOAPNOYDP
XSHPBAAQDRRNLVLSEMKNQSTSAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYL
KEVINQYEQGETGYNLLTTGMDYYTNNDQEACKHUMDTINSDQYYSYDDBLQVASTVV
DVSNGKVIAQLGARHQASNYSTNNDQEACKHUMDTINSDQYYSYDDBLQVASTVV
DVSNGKVIAQLGARHQASNYSTNNDRAYFONITLQYADQSRWYAPTIDYAPAIEYGVYDSTAT
MVNDIPYNYPGTSTPPYYNWDRAYFGNITLQYALQGSRWYTAVETLNKVGEDRAKTFLN
GLGIDYPSMHYANAISSNTTESNKQYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
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pneumoniae isolated
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                                                         ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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FRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ponA gene
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Genetik, Ihnestr. 73, 1000 Berlin 33,
2 (bases 1 to 2157)
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93010977
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ponA gene f
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Streptococcus pneumoniae.
Streptococcus pneumoniae
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/clone="pcMK1-pcMK16"
1. .2157
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/transl_table=11
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1. .>2157
/gene="ponA"
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X67869
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Hakenbeck, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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TITLE
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Streptococcus.

(bases 1 to 2160)

(offeyy.T.J. Daniels,M., Enright,M.C. and Spratt,B.G.

Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
99392464
                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="pbpla"
/function="peptidoglycan transglycosylase-transpeptidase"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                      /serotype="9V"
/db_xref="taxon:1313"
/note="Spanish member of the major penicillin-resistant
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                                                                                                                                                                                                     2 (bases 1 to 2160)
Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for the
Epidemiology of Infectious Disease, Department of Zoology,
University of Oxford, South Parks Road, Oxford, Oxfordshire
3PS, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 TAAAATCTACGACAATAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA
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pred. No. 1.3e-167;
0; Mismatches 7;
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m Nard, C., Ouellette, M.,
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                                                                              Location/Qualifiers
1. -2157
Arganism="Streptococcus pneumoniae"
/strain="670"
 Bergeron, M.G., Boissinot, M., Huletsky, A.,
                                                                                                                                                                                                     Score 318; DB 6; 1
Pred. No. 1.3e-167;
0; Mismatches 7;
           Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to
for detection of microorganisms
Patent: WO 0123604-A 2140 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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/tdncton="peptidogijycan tiquisgijycusyitase tiquispeptidasse=
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/prodeut="penicallin-binding protein la"
/prodeut="penicallin-binding protein la"
/prodeut="penicallin-binding protein la"
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/db_xref="id="AADA 306.1"
/db_xref=
                                   /gene="pbpla"
/function="peptidoglycan transglycosylase-transpeptidase"
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Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus penumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Submitted (31-MAR-1999) The Wellcome Trust Centre for the Epidemiology of Infectious Disease, Department of Zoology, University of Oxford, South Parks Road, Oxford, Oxfordshire OX1 3PS, UK
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/organism="Streptococcus
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G. Serotype 14 variants of the Spanish penicillin-resistant serotype 9V clone of Streptococcus penumoniae arose by large recombinational replacements of the cpsA-pbpla region Microbiology 145 (Pt 8), 2023-2031 (1999)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                            TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC
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                                                                                                                           TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA
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Coffeyr, J., Daniels, M., Enright, M.C. and Spratt, B.G.
Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for
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LSEGSNNDEMNIPGLYRNGEFFRINGARSTWSSPRQQPPSTESSSSSSSSSSSSSSS
                                                                                                                 Streeptococcus pneumoniae strain PO-341 penicillin-binding protein AF139885
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
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Spanish serotype 9V clone"
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Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for the
Epidemiology of Infectious Disease, Department of Zoology,
University of Oxford, South Parks Road, Oxford, Oxfordshire OXI
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/strain="PO-341"
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Epidemiology of Infectious Disease, Department of Zoology

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Spanish serotype 9V clone"
University of Oxford, South Parks Road, Oxford, Oxfordshire OX1 3PS, UK
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/protein_id="AAD43069.1"
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Pred. No. 1.3e-167;
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                                         /organism="Streptococcus/strain="PO-342"
                                                            /serotype="14"
/db_xref="taxon:1313"
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
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KEVINQVEQETGYNLLTTGMDVYTNVDQEAQKHLWDIYNSDQYVSYPDDDLQVASTVV
DVSNGKVIAQLGARHQASNVSFGTNQAVETNRDWGSAMKPITDYAPAIEYGVYDSTAT
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GLGIDYPSMHYANAISSNTTESNKQYGASSEKMAAAYAAFANGGTYYKPWYIHKVVFS
DGSKKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRGAYLPWLPQAGKTGTSNYTDE
EVENHIKNTGYVAPDEMFVGYTRKYSMAVWTGYSNRLTPIVGDGFLVAAKVYRSMITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G. Direct Submission Submitted (31-MAR-1999) The Wellcome Trust Centre for the Epidemiology of Infectious Disease, Department of Zoology, University of Oxford, South Parks Road, Oxford, Oxfordshire OXI 3PS, UK
                                                                                                                                            ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA
AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACGCCGGAAACTTGGTCTT
                                                                                                                 ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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/organism="Streptococcus pneumoniae"
/strain="M134"
/serotype="14"
/db_xref="taxon:1313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae strain. (pbpla) gene, complete cds.
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1. .2160
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Serotype 14 variants of the Spanish penicillin-resistant serotype 9V clone of Streptococcus pneumoniae arose by large recombinational replacements of the cpsA-pbpla region Microbiology 145 (Pt 8), 2023-2031 (1999)
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/transl_table=11
/product="perioding protein la"
/protein_id="AAD43071.1"
/db_xref="GI:5410467"
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KEVINQVEQETGYNLTTGMDVYTNVDQEAQKHLWDIYNSDQYVSYPDDDLQVASTVV
DVSKOKYLAQLGARHQASNYSFGTNQAVETNRNWGSAKKPITDYAPAIEYCOYYDSTAYY
MYNDIPYNYPGTSTPVYNWDRAYFRONITLOYARLQSAKNYTAVETLNYGLDRAKYFLN
GLGIDYPDMYANNISSNYGYGASSEKNAAAYAAFANGGYYYKPYNTHVVYFS
DGSKKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRGAYLPWLPQAGKTGTSNYTDE
EVENHIKNTGYYAADDEMFVOYTRKYSMAVMTQYSNRLPIVGDGFLVAAKYYRSMTTY
LSEDTHPEDWTMPDGLFRNGEFYFKNGARSTWNSPAQQPPSTESSSSSDSSTSQSS
STTPSTNNSTTNRNNTQGSNTTPDQQNQNDQPAQP*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Uruguayan variant of the major penicillin-resistant
Spanish serotype 9V clone"
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                                                                                                                           10463168

2 (bases 1 to 2160)

2 (offey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.

Direct Submission

Submitted (31-MAR-1999) The Wellcome Trust Centre for the

Epidemiology of Infectious Disease, Department of Zoology,

University of Oxford, South Parks Road, Oxford, Oxfordshire OX1
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    .2160
/organism="Streptococcus pneumoniae"
/strain="URU-E135"

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                                                                                                                                                                                                                                                                                                                                                                                                                         /serotype="14"
/db_xref="taxon:1313"
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/gene="pbpla"
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            LSEDTHPEDWTMPDGLFRNGEFVFKNGARSTWNSPAPQQPPSTESSSSSSDSSTSQSS
STTPSTNNSTTINPNNNTQQSNTTPDQQNQNPQPAQP"
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penicillin-binding protein
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Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                          Score 318; DB 1;
Pred. No. 1.3e-167;
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Streptococcus pneumoniae strain URU-E135 |
1a (pbpla) gene, complete cds.
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BCT 26-AUG-1999
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(bases 1 to 2160)

(Offey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.

Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-phpla region

Microbiology 145 (Pt 8), 2023-2031 (1999)
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Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for the
Epidemiology of Infectious Disease, Department of Zoology,
University of Oxford, South Parks Road, Oxford, Oxfordshire OX1
3PS, UK
                                   420
                                                                             540
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                                                                                          GGTCTACATGTCTAATGGGAACTATGGAATGCAGCAGCAGCTCAAAACTACTATGGTAA
                                                                                                                                     /product="penicillin-binding protein la"
/protein_id="AAD43072.1"
/db_xref="G1:5410469"
                                                                                                                                                                                                                                                                                                                                                               la (pbpla) gene, complete cds.
AF139889
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// function="poptidoglycan transglycosylase-transpeptidase"
// codon_start=1
// transl_table=11
// product="penticillin-binding protein la"
// protein_id="Aabd3073.1"
// protein_
                                                                                                                                                                                             Streptococus.

(bases 1 to 2160)

(offey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.

Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
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Spanish serotype 9V clone"
  pneumoniae strain URU-E159 penicillin-binding protein
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Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for the
Epidemiology of Infectious Disease, Department of Zoology,
University of Oxford, South Parks Road, Oxford, Oxfordshire OX1
3PS, UK
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/strain="URU-E159"
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Streptococcus pneumoniae strai
la (pbpla) gene, complete cds.
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Matches 668;
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Serotype 14 variants of the Spanish penicillin-resistant serotype
Serotype 14 variants of the Spanish penicillin-resistant serotype
V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (1999) In press
2 (bases 1 to 2160)
Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Direct Submission
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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/note="variant of the major penicillin-resistant Spanish
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                                                                                                 TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC

    2160
    /organism="Streptococcus pneumoniae"

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/db_xref="taxon:1313"
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AF159448
AF159448.1 GI:5726354
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1. .2160
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                                                                                                                                             /product="panietilin-binding protein la"
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Pred. No. 1.3e-167;
0; Mismatches 7; Indels
                                                                                                          /codon_start=1
/trans1_table=11
                  /gene="pbp1a"
1. .2160
                                                               /gene="pbpla"
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99.0%;
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/GGGOD_SELECT-1
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/CEGGOSTGOD_SERECT-1
/CEGGOSTGOD_SERECT
2160 bp DNA linear BCT 17-SEP-2001 Inceptococcus pneumoniae isolate SP 1053 penicillin-binding protein AF210749.1 GI:6563344
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[ (bases 1 to 2160)
Ferroni, A. and Berche, P.
Alterations to penicillin-binding proteins 1A, 2B and 2X amongst
penicillin-resistant clinical isolates of Streptococcus pneumoniae
serotype 23F from the nasopharyngeal flora of children
J. Med. Microbiol. 50 (9), 828-832 (2001)
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Ferroni, A. and Berche, P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospital
Necker-Enfants-Malades, 149 rue de Sevres, Paris 75015, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120
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/organism="Streptococcus pneumoniae"
/serotype="23F"
/isolate="SP 1053"
/db xref="taxon:1313"
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llarity 99.0%; Pred. No. 1.3e-167;
Conservative 0; Mismatches 7;
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TGCCCAAGCTAATGATATCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120
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            /db_xref="taxon:1313"
                                                         /gene="pbpla"
                                   /gene="pbpla"
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Farzoni, A. and Berche, P.
Alterations to penticillin-binding proteins 1A, 2B and 2X amongst penticillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23F from the nasopharyngeal flora of children J. Med. Microbiol. 50 (9), 828-832 (2001)
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Ferroni,A. and Berche,P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospital
Necker-Enfants-Malades, 149 rue de Sevres, Paris 75015, France
Location/Qualifiers
1. 2160
219 TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACA 278
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/serotype="23F"
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/product="penicillin-binding protein 1A"
/product="penicillin-binding protein 1A"
/protein_id="AAF17261.1"
/db_xref="61:6563349"
/db_xref="61:656349"
/db_xref="61:6563349"
/db_xref="61:6663349"
/db_xre
                                                                                                                                                                                                                    Streptococcus pneumoniae isolate SP 22861 penicillin-binding protein 1A (pbpla) gene, complete cds.
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DGSKKEFSDVGTRAMKETTAYMMTEMMKTVLAYGTGRGAYLPWLAQAGKTGTSNYTDD
EIEKHIKNTGYVAPDEMFVGYTRKYSMAVWTGYSNRLTPIVGDGFLVAAKVYRSMITY
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1 (bases 1 to 2160)
Ferroni,A. and Berche,P.
Alterations to penicilin-binding proteins 1A, 2B and 2X amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23F from the nasopharyngeal flora of children J. Med. Microbiol. 50 (9), 828-832 (2001)
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Ferroni, A. and Berche, P.
Direct Submission
Submitted (03-DEC-1999) Microbiology, Hospital
Necker-Enfants.Malades, 149 rue de Sevres, Paris 75015, France
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Pred. No. 1.3e-167;
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/organism="Streptococcus pr
/serotype="33F"
/isolate="SP 22861"
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/codon_start=1
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Bacteria; Firmicutes: Bacillus/Clostridium group; Streptococcaceae;
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1 (bases 1 to 2160)

Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Pidard,F.J. and Roy,P.H.

Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Fatent: Wo 0123604-A 1169 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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                                                                     339 TCTGCAAAGTAATTCCCTCCAAGGTGGATCAACTCTCACCAACAGTTGATTAAGTTGAC
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/strain="SP-665"
/db_xref="taxon:1313"
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Length 2160;

DB 6;

15.9%; Score 318;

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          Indels
 Pred. No. 1.3e-167;
0; Mismatches 7;
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Best Local Similarity 99.0%;
Matches 668; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protect can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection enpneumonia, otitis media or meningitis, probes based on the nucleic ac
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                                                                                                                                                                                                                                                                                                                                                                             Barash
Kunsch
                                                                                                                                                                                                                                                                  Computer-readable medium polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae; S. pneumoniae; computer readable medium; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1981
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                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
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                                                                                                                                                                                                                      pneumoniae
                                                                                                                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttctacgtggaactcacctgctccacaaccacccccatcaactgaaagttcaagctcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggctgtatggacaggctattctaaccgtctgacaccacttgtaggcaatggccttacggt
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                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                             SC,
                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                             Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                           972-978; 1409pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae
                                                                                                                                                                                                                                             compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             SCI
                                                                                                                                                                                                                                                                                                                                                                                                  Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10711
                                                                                                                                                                                                                                           with recorded Streptococcus pneumoniae - useful in diagnostic kits and assays, ons and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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ccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                  ЪJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                  Dougherty
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                                                                                                                                                                                                                                                                                                                                                                                                    Fannon
                                                                                                                                                                                                                                                               assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assay;
on; ds.
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV22134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted SEQ ID NO:1 to 391 (AAV52334 to AAV52524) are genomic fragments from SEQ ID NO:1 to 391 (AAV52334 to AAV52524) are genomic fragments from

95**8** 

SEQ ID NO:1 to 391 (AAV52134 t Streptococcus pneumoniae. The

nucleic

molecule

encoding

b

homologue

present invention also describes

CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule is produced by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO:1 to 391, identifying members of the CC isolating the nucleic acid molecules from the members; or (b) isolating CC mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid CC molecules whose nucleotide sequence is homologous to amplification CC primers derived from the fragment of the S. pneumoniae genome to prime CC the amplification and isolating the amplified sequences. The computer CC readable medium can be used in a computer-based system for identifying CC from the present invention can be used in diagnosis kits and assays, and CC pharmaceutical compositions and vaccines for S. pneumoniae.

999999999999999888

Sequence 10711 BP; 3280 A; 2056 C; 2412 G; 2963 Τ; 0 other;

	780	AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT	721	Qy
	9048	TAATTACCTCANGGAAGTCATCAATCAAGTTGAAGAAGAACAGGCTATAACCTACTCACTACTCACTAGTTAACTTACCTCAAGAAGAAGAAACAGGCTATAACCTACTCACTAATTACCTCAAGAAGAAGAAACAGGCTATAACCTACTCAC	9107	DP CA
	, c	ACCAMITACIONISCACIACAMANDICICAMANICAGCAMATAACICATTACATIGGA	7107	? 5
		ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA	601	, Q
	9168	ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATA	9227	В
	600	ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC	541	Qy
	9228	AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT	9287	Дb
	r 540	AAACCAATATGACCCCTATTCACATCCAGAAGCCAGCCCAAGACCGCCGAAACTTGGTCTT	481	Qy
	9288	AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	9347	망
	480	AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	421	Qy
	9348	GTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCTCAAAACTACTATGGTAA	9407	Дb
	420	GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA	361	Qy
	9408	AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAATAA	9467	ф
	360	AGCGATTCAGTTAGAACAAAAAGCAAGCAAGCAAGAAATCTTGACCTACTATATAAATAA	301	Qy
	9468	TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT	9527	рь
	T 300	TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT	241	Qγ
	9528	TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC	9587	Db
	240	TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC	181	Qy
	9588	TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA	9647	Db
	180	TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA	121	Qy
	1 9648	TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA	9707	DЪ
	120	TGCCCAAGCTAATGATATTCCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA	61	Qy
	A 9708	TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA	9767	DЬ
	1 60	TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA	1	Qy
0,	Gaps	atch 100.0%; score 1999; DB 19; Length 10711; cal Similarity 100.0%; Pred. No. 0; 1999; Conservative 0; Mismatches 0; Indels 0;	Query Match Best Local Matches 199	<b>7</b> H O
		100 00 71 1000 71 10		

1860	TTCTACGTGGAACTCACCTGCTCCACAACAACCACCCCATCAACTGAAAGTTCAAGCTCATC	1801	Qy
7908		7967	Db
1800	TTGGAATATACCAGAGGGGCTCTACAGAAATGGÁGAATTCGTATTTAAAAATGGTGCTCG	1741	Qу
7968		8027	Дъ
1740	CTGAAGGAAGCAATCCAGAAGA		Qy
8028			Db
1680	GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT	1621	Qy
8088		8147	Db
1620 8148	GACCICTCAAITTGTAGCACCIGATGAACTAITTGCIGGCTATACGCGTAAATAITCAAI	1561 8207	ОУ
1560	TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA	1501	ДУ
8208		8267	
1500 8268	CATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	1441 8327	ДУ
1440	AACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGA		Оу
8328			Дъ
1380	TGGAACTTACTATAAACCAATGTATATGCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA		Qу
8388			Дъ
1320	CAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTACGCTGCCTTTGCAAATGG		Qy
8448			Db
1260	AATCGACTACCOAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA	1201	Qy
8508		8567	Db
1200	CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAGG	1141	Qу
8568		8627	
1140	GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC	1081	Qy
8628		8687	Db
1080	CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG	1021	Qy
8688		8747.	Db
1020 8748	ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT	961 8807	Qу
960	TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATGAA	901 8867	Qy Db
900	TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA	841 8927	Qу
840 8928	TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT	781 8987	Qу
8988	AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT	9047	DЪ

Score

DB

17;

Length

0

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RESULT
ADATO8027
IDT 0827
XX AATO
XX AATO
XX Pen
CX XX Pen
KW CTAI
KW ACL
XX ACL
PT CDS
YX CAL
PT OPT
PR 01-
XX ACL
PT OPT
PR 01-
XX ACL
PT OPT
PT OPT
YX ACL
YX AC
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                                                                The present sequence encodes a soluble variant of the S. pneumoniae penicillin binding protein (PBP) 1A, which lacks the 1st 38 amino acid residues of the wild type protein. Wild type PBP is a bifunctional protein, which binds the cell membrane when expressed in a bacterial cell, having transplycosylase and transpeptidase activities. The variant protein (NCIMB 40665) in conjunction with a labelled anti-bifunctional PBP monoclonal antibody, can be used to identify and assay for cpds. which bind bifunctional PBP. Such cpds., as inhibitors of bifunctional PBP have a potential use in therapeutic cpds. which inhibit the growth of antibiotic resistant pacteria. The soluble variant may also be used in x-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transglycosylase; transpeptidase; identification, antibiotic resistant; bacteria; soluble variant; X-ray crystallography; determination; ds.
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                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-1994;
01-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                              for antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penicillin
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                                                                                                                                                                                                                                                                                                                                                                                                            derivs. of bifunctional penicillin binding protein lack transglycosylase activity, useful to identify antibodies or cpds. which bind BPBPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1996-042232/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCAACCAGCACAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCAACCAGCACAACCA
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                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         penicillin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94SE-0004072
94IN-0000580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                 65-68;
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Matches Query Match Best Local

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The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes cand/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical especies with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more cused for producing probes and/or primers for detecting one or more cused for producing probes and/or primers for detecting one or more cused for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal customatical species, genus, family and group. A nucleic acid (1) cobtained using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at cleast one toxin gene. hexA nucleic acids are used for the specific and cubiquitous detection and for identification of Streptococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., corynebacteriaceae family, Pseudomonads group, Streptococcus sp. (2) Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can company to the specific and couracy is also achieved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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CC Note: The sequence data for this patent did not form part of the printed encorification but the Obstained in alternation.
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26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic cids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacterial, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cleast one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp., CC corynebacteriaceae family, Pseudomonads group, Escherichia coli, CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests CC provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
Sequence 1249
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1214; Conserv
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                                                                  GGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAATGTTTCCTTCGGAATT
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TACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGACGAA 796

tacacaaatgtagaccaagaagctcaaaaacatctgtgggatatttacaatacagacgaa

162 736 CTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGATAATTACCTCAAGGAA 676

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977 343 917

GCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTATCGTTCACGATGAGCCC aaccaagcagtagaaacaaaccgcgactggggatcaactatgaaaccgatcacagactat AACCAAGCAGTAGAAACCAAACCGCGCACTGGGGATCAACTATGAAACCGATCACAGACTAT ggtaaagtcattgcccagctaggagcacgccatcagtcaagtaatgtttccttcggaatt GGTAAAGTCATTGCCCCAGCTAGGAGCACGCCATCAGTCAAGTAATGTTTCCTTCGGAATT

402

342 916 Qy

677

Вb QΥ

43

Matches

1190;

Conservative

0;

Mismatches

5

Indels

0;

Gaps

0

Similarity

617

QУ Ъ

737 103

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CC A polymerase chain reaction (PCR) assays have been developed for CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC and the pbp1A gene. The products and methods can be used for detecting CC S. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and CC identifying any antibiotic-resistant S. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains in a sample. CC The assays can be used to detect other pathogens causing meningitis. CC The assays can be used to detect other pathogens causing meningitis. CC The assays can be used to detect an antibiotic resistant strain of CC S. pneumoniae with a minimum inhibitory concentration (MIC) of CC S. pneumoniae with a minimum inhibitory concentration and DC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and CC a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
Query Match
Best Local
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                         Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAME-)
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UNIV WITWATERSRAND.
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                                                                                                                                                                                                                                                                                                                                                                   diagnosis
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of pneum
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Score 940;
Pred. No. 0;
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                                                    identification; pneumococcal meningitis; ss.
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                                                                              penicillin binding
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Query Best L

Best Local Similarity Matches 1253; Conserv

Conservative

0;

Pred.

ed. No. 0; Mismatches

DΒ

Length Indels

0;

Gaps

0,

45.2**%**; 99.4**%**;

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A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting S. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and clentifying any antibiotic-resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be used to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of O.25-I micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SAME-)
(UYWI-)
(MEDI-)
                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 4; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                               Polymerase chain reaction useful for the diagnosis
                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-601770/51
                                                                                                                                                                                                                                                                                                                                                                                                                                       Klugman
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MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith
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                                                                           ctaggagcacgccatcagtcaagtaatgtttccttcggaattaaccaagcagtagaaaca
                                                                                       CTAGGAGCACGCCATCAGTCAAGTAATGTTTCCTTCGGAATTAACCAAGCAGTAGAAACA
                                                                                                                               gatgaattgcaagtcgcttctaccattgttgatgtttctaacggtaaagtcattgcccag
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GGTGTCTACGATTCAACTGCTACTATCGTTCACGATGAGCCCTATAACTACCCTGGGACA 1054
                       aaccgcgactggggatcaactatgaaaccgatcacagactatgctcctgccttggagtac
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The assays can be adapted to detect other pathogens causing meningitis. The assays can be used to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbplA transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
                                                                                                                                                      A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbplA gene. The products and methods can be used for detecting S. pneumoniae, particularly antibiotic resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and identifying any antibiotic resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant
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                         ggtaaagtcattgcccagctaggagcacgccatcagtcaagtaatgtttccttcggaatt
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A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and cidentifying any antibiotic-resistant s. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be used to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of s. pneumoniae with a minimum inhibitory concentration (MIC) of 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
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This sequence represents the DNA encoding exp2. This sequence is identical to that for ponA which encodes penicillin-binding protein (Pbpla). The protein encoded by this sequence is involved in adhesi of bacteria to target cells. This sequence encodes an exported prot
                                                      Claim
                                                                                   Novel
                                                                                                                                      Masure
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                                                                                                                                                                               01-SEP-1993;
18-MAY-1994;
                                                                                                                                                                                                            01-SEP-1994;
                                                                                                                                                                                                                                                                                                      Exp2; export protein; permease like protein;
penicillin binding protein 1A; pbpla; plpA; exp1; exp3;
pyruvate oxidase; virulence determinant; regulatory elem
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DB; AAR70153.
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94US-0245511
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TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAGAACAGGCTATAACCTACTCAC
                                                                                                               ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                                                                                                                                        GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA
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                                                AACTGGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT
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                                      aactgggatggatgtctacacaaatgtagaccaagaagctcaaaaacatctgtgggatat
                                                                           taattacctcaaggaagtcatcaatcaagttgaagaagaaacaggctataacctactcac
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46; Conservative
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RESULT 1
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                                                                                                                                                                                              CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC and the pbp1A gene. The products and methods can be used for detecting CC s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and CC The methods can be used for detecting S. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains resistant CC The assays can be adapted to detect other pathogens causing meningitis. CC The assays can be used to detect other pathogens causing meningitis. CC The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
                                                              Matches
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                                                                                                                                                               Sequence
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                                                                                Local Similarity
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GAACAGTATGAGAAAGCAGTCAATACACCAATTACTGATGGACTACAAAGTCTCAAATCA
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                                                              Conservative
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Streptococcus pneumoniae; penicillin binding protein; pbp2B; transpeptidase encoding region; TER; antibiotic resistance; detection; identification; pneumococcal meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC A polymerase chain reaction (PCR) assays have been developed for CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC and the pbp1A gene. The products and methods can be used for detecting CC s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and CC identifying any antibiotic-resistant s. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. CC The assays can be used to detect other pathogens causing meningitis. CC The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of C 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and CC 0.25-1 micro g/ml transpeptidase encoding region (TER) isolate nucleotide concentration the present sequence represents a Streptococcus cous sequence from the present invention.
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                                                                                                                                                                                                                                                                                   Species specific; genus specific; family specific; identification; algal; archaeal; bacterial; fungal
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oy PH;
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Nucleic acid sequences are us primers which can be used to archaeal, bacterial, fungal a

es are used to generate universal probes and used to identify and detect the presence of algorizational and parasitical species in a test sample

of algal,

Disclosure; Page 1468; 1580pp;

English

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related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC and parasitical species, genus, family and group. A nucleic acid (I) CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antimicrobial agent resistance gene or at CC least one toxin gene. hexA nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group CC which can be detected include Abiotrophia adiacens, Bordetella sp., CC wycobacterium sp., Enterobacteriaceae group, Escherichia coli, CC Mycobacteriaceae family, Pseudomonads group, Escherichia coli, CC wisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests CC provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes CC which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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TTTGCAAATGGTGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGAT
                                                                                                                                                                                                                                                                                                                                        AACGTCCCAGCCGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTA
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                                                                                                                  ACCGAATCAGACAAAAAATATGGAGCAAGTAGTGAAAAAGATGGCTGCTTACGCTGCC
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Pred. No. 0;
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                                                                           related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and biquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species specific; genus specific; family specific; probe; dete identification; algal; archaeal; bacterial; fungal; parasitica microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobia
                            Corynebacterium : Mycobacteriaceae
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ily, Pseudomonads group,
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Tolle, Streptococcus
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Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests ovides faster results than substrate specificity tests as results can determined in an hour and improved accuracy is also achieved. HO0010 to AAH002304 represent nucleotide sequences and primers/probes ich are given in the exemplification of the present invention.
                                                                                                                                                              TACGCTGCCTTTGCAAATGGTGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTC
                                                                                                                                                                                                                                                                                                                                                          ACTTTCCTAAATGGTCTAGGAATCGACTACCCAAGTATTCACTCAAATGCCATTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGTTTATAACTGGGATAGGGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAA
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                                                                                                                                                                                                                                        TTTAGTGATGGGAGTGAAAAAGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACG
                                                                                                                                                                                                                                                             tacgctgcctttgcaaatggtggaacttactataaaccaatgtatatccataaagtcgtc
                                                                                                                                                                                                                                                                                                             agtaacacaaccgaatcagacaaaaaatatggagcaagtagtgaaaagatggctgctgct
                                                                                                                                                                                                                                                                                                                                                                                                          caatcgcgaaacgtcccagccgtggaaactctaaacaaggtcggactcaaccgcgccaag
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     pneumoniae;
                             pneumoniae pbp1A TER isolate
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Pred. No. 4.1e-294;
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                           9)
     protein; pbp2B; pbp1A;
                             nucleotide
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cc detecting an antibiotic resistant strain of Streptococcus pneumoniae cusing primers based on the penicillin binding protein 2B (pbp2B) gene can the pbp1A gene. The products and methods can be used for detecting S. pneumoniae, particularly antibiotic resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and compared to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be used for detecting S. pneumoniae strains meningitis. CC The assays can be adapted to detect other pathogens causing meningitis. CC The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and CC a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide concentration the present invention.
(SAME-)
(UYWI-)
(MEDI-)
                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                               Polymerase chain reaction assays for detecting Streptococcus useful for the diagnosis of pneumococcal meningitis \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transpeptidase encoding region; TER; antibiotic resistance; detection; identification; pneumococcal meningitis; ss.
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nes 681; Conserv
                                                                                                                                                                                                                                                                                                                             AACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAGGGGCTACTTTGGCAACATC
                                                                              CCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTATCGTTCACGATGAGCCCTAT
                                                                                                                                             CAAGCAGTAGAAACCAAACCGCGACTGGGGATCAACTATGAAACCGATCACAGACTATGCT
                                                                                                                                                                                                                GTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCATTGTTGATGTTTCTAACGGT
aactaccctgggacaaatactcctgtttataactgggataggggctactttggcaacatc
                                                                                                                                                                                             aaagtcattgcccagctaggagcacgccatcagtcaagtaatgtttccttcggaattaac
                                                                                                                                                                                                                                                              gttgcctatccagacgatgaattgcaagtcgcttctaccattgttgatgtttctaacggt
                                                                                                                                                                                                                                                                                                                                                               ACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGACGAATAC
                                                             cctgccttggagtacggtgtctacgattcaactgctactatcgttcacgatgagccctat
                                                                                                                              caagcagtagaaacaaaccgcgactggggatcaactatgaaaccgatcacagactatgct
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Score 581; DB 20;
Pred. No. 1.8e-289;
0; Mismatches 2;
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Query Match Best Local Matches

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Length 1260; Indels

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The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more
                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                             Nucleic acid seque 
primers which can
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19-MAY-2000; 2000CA-2307010
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergeron MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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bacterial,
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parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microorganisms e.g. algae, es, for universal detection
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Sequence 1229 B₽; 399 Α; 287 0 240 G; 303 Η, 0 other;

Query Match Best Local Matches

Similarity

28.4%; 99.7%;

DB 22; 3.1e-282;

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                                     TATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAAAGAGTTCTCTAATGTCGGAACTCG
                                                                           aaagatggctgcttacgctgcctttgcaaatggtggaacttactataaaccaatgta
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                       tatccataaagtcgtctttagtgatgggagtgaaaaagagttctctaatgtcggaactcg
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                                                                                                                                                                                                                                      A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting S. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococal meningitis and identifying any antibiotic-resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAME-)
(UYWI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; penicillin binding protein; pbp2B; transpeptidase encoding region; TER; antibiotic resistance; detection; identification; pneumococcal meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                               28-APR-1999
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                                                                                                                                                                                           .25-1 micro g/ml where the PCR products detected are a 1043 bp and 224 bp product. The present sequence represents a Streptococcus neumoniae pbplA transpeptidase encoding region (TER) isolate nucleotide squence from the present invention.
 1999-601770/51
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                (SMIK ) SMITHKLINE BEECHAM CORP
                                               16-AUG-1996;
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Query Match
Best Local Similarity
Matches 811; Conser
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nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungil and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae.
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AANO0101 to AANO02304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
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                             TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAAC
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consider the method of the invention can be used for the universal detection of at least one at least one at least one toxin gene or at least one toxin gene or at least one of the specific and universal detection and for specific and ubiquitous detection of any bacteriam, fungiand constant of any bacteriam, fungiand gene or at least one antimicrobial agent resistance gene or at least one antimicrobial agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., corynebacteriam sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Escherichia coli, consisted in an hour and improved accuracy is also achieved.

Chahloolo to Abhooloud the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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                                                                                                                                                                                    microorganism; diagnosis; translation elongation factor Tu; tc translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrohivaccine; primer; ds.
                                                                                                                                  WO200123604-A2
                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                    Species specific;
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 (INFE-) INFECTIO DIAGNOSTIC (IDI) INC
                             28-SEP-1999;
19-MAY-2000;
                                                                         28-SEP-2000;
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      Boissinot
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      Huletsky
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       Menard
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       Ouellette
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Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test sa a test sample algal,

1580pp; English.

Species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more related microorganisms e.g. alyae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous context detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) cobtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cotation of any bacterium, fungus or parasite in a sample and for the cotation of the last one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptcocccus sp., Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention. nucleic acids of tuf, fus, atpD and/or recA genes from which pro and/or primers are derived. The method comprises amplifying the acids of determined algal, archaeal, bacterial, fungal and parasections of determined algal, archaeal, bacterial, bacterial, archaeal, bacterial, bacterial, archaeal, bacterial, bacteria The present invention describes nucleic acids of tuf, fus, atpD a method for generating a repertory parasitical probes nucleic

Sequence 2160 ₿P; 869 A; 494 C; 403 **G**; 565 T; 0 other;

Length

2160;

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Query Match
Best Local Similarity
Matches 668; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species specific; genus specific; family specific; probe; deterior identification; algal; archaeal; bacterial; fungal; parasitica microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPAGE.
The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recR genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal
                                                                                                                                                                                                                                                                                                                         Disclosure;
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Picard FJ,
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                    Page 1464-1465;
                                                                                                                                                                                                                                                                                                                                                                   sequences are used to generate universal probes and be used to identify and detect the presence cterial, fungal and parasitical species in a test
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection of any bacterium, fungus or parasite in a sample and for the cd detection of at least one antimicrobial agent resistance gene or at clast one toxin gene. hexA nucleic acids are used for the specific and cubiquitous detection and for identification of Streptococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Corynebacteriaceae and Staphylococcus sp., Using DNA based tests concept for the specificity tests as results can be determined in an hour and improved accuracy is also achieved.

Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Corynebacteriaceae and Staphylococcus sp., Using DNA based tests corynides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

Corynebacteriaceae family are present nucleotide sequences and primers/probes contains and primers and primers and primers are given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                    0.25-1 micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbplA transpeptidase encoding region (TER) isolate nucleo
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and the pbplA gene.
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                                                                                                                                                                                                                                                Sequence 1260 BP;
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                                                                                                                                            GAACAGTATGAGAAAGCAGTCAATACACCAATTACTGATGGACTACAAAGTCTCAAATCA
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                                                                                         gaaccagtatgagaaagcagtcaataccaccaattactgatggactacaaagtctcaaatca
 GAAGCTCAAAAAACATCTGTGGGATATTTACAATACAGACGAATACGTTGCCTATCCAGAC
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumococcal meningitis
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Pred. No. 8.3e-127;
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        The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species specific; genus specific; family specific; probe; detection identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                               Nucleic acid sequences are used to generate universal probes primers which can be used to identify and detect the presence archaeal, bacterial, fungal and parasitical species in a test
                                                                                                                                                                                                                      Disclosure;
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19-MAY-2000;
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                                                            Polymerase chain reaction useful for the diagnosis
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Fig 4; 63pp;
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Pred. No. 3.5e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A polymerase chain reaction (PCR) assays have been developed for CC detecting an antibiotic resistant strain of Streptcoccus pneumoniae cu using primers based on the penicillin binding protein 2B (pbb2B) gene CC and the pbplA gene. The products and methods can be used for detecting CS. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and CC identifying any antibiotic-resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. CC The assays can be adapted to detect other pathogens causing meningitis. CC The assays can be used to detect an antibiotic resistant strain of CS. pneumoniae with a minimum inhibitory concentration (MIC) of CS. pneumoniae with a minimum inhibitory concentration (MIC) of CS. pneumoniae phplA transpeptidase encoding region (TER) isolate nucleotide CC pneumoniae phplA transpeptidase encoding region (TER) isolate nucleotide
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translation elongation factor G; RecA recombinase; resistance;
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                                                                                                                                                                  ; family specific; bacterial; fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 Т;
                                                                                                                       ATPase; antimicrobial;
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Best Local s
Matches 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be accounted and contrary is also achieved.
                                                                                                                                                                                         1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous
                                                                                                                                                                                                                                                             1044
                                   AAH01025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1212 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 1470; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences are used to generate universal primers which can be used to identify and detect the 
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Picard FJ,
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                                   DNA;
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                                     1222 BP
                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DE Pred. No. 2.3e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 G;
                                                                                                                                                                                                                                                                                                                                                                                                              3 178;
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Query Match Best Local S Matches 228

Similarity

8.98;

Pred. No. 2.3e 0; Mismatches

DB 22; .3e-81;

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Gaps

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Conservative

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related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and biquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp., or parasite of the contraction of the contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification; algal; archaeal; bacterial; fungal; parasıtıca microorganism; diagnosis; translation elongation factor Tu; translation elongation factor G; Reck recombinase; resistance; translation elongation factor G; Reck recombinase; resistance;
                                                                                                                                  Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based te provides faster results than substrate specificity tests as resu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test sa
Sequence
                                                  \Delta AAH00010 to \Delta AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1999;
19-MAY-2000;
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                                                                                                              determined in an hour and improved accuracy is also achieved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 969-970; 1580pp; English.
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233 G;
330 T; 0
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RESULT 3
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                                                                                                                                                                                          and/or primers are derived. The mechanical and parasitical acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal obtained using the method of the invention can be asample and for the
                     detection of any bacterium, fungus or parasite in sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hava nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal. harterial functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bergeron M
Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; Page 967-968; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1999; 99CA-2283458
19-MAY-2000; 2000CA-2307010
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                                                                                                                                                     Nucleic
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to identify and detect the p
                                                                                                                                                                                                                                                                              Huletsky A,
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                Ouellette
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Claim 27;

Page 1474-1475; 1580pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical Species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC used for producing probes and/or primers for detecting one or more CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antinicrobial agent resistance gene or at CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC unicroorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., CC Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., CC Nelsseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests CC provides faster results than substrate specificity tests as results can be used for the specific and increase and improved accuracy is less as increase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                   identification; algal; archaeal; bacterial; fungal; parasitics microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance;
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                                                                                                                                                                                                                                translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH01021 standard; DNA; 1201
               28-SEP-1999;
19-MAY-2000;
                                                                                                                                           WO200123604-A2
                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                        Species specific;
                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                   28-SEP-2000;
                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATAATACGCAACAATCAAATACAACCCCTGATCAACA 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGACTACCAATCCTAA 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcacctgctccacaacaaccccccatcaactgaaagttcaagctcatcatcagatagttc 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCATCATCAGATAGTTC 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caataatacgcaacaatcaaatacaacccctgatcaaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                 primer;
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               99CA-2283458
2000CA-2307010
                                                                   2000WO-CA01150
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                                                                                                                                                                             pneumoniae
                                                                                                                                                                                                                                                                                                                                            pneumoniae nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the exemplification
                                                                                                                                                                                                                                                                                                          genus specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 A; 270
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Pred. No.
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                                                                                                                                                                                                                                                                                       ; family specific; probe;
bacterial; fungal; paras;
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                                                                                                                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                       parasitical;
                                                                                                                                                                                                                                                                                                                                              NO:1012
                                                                                                                                                                                                                                                                      Tu; toxin;
                                                                                                                                                                                                                                                                                                          detection;
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cc acids of determined algal, archaeal, bacterial, fungal and parasitical cospecies with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc related microorganisms e.g. algae, archaea, bacteria, fungi and combinations of an algae, archaeal, bacterial, fungi and comparasities, for universal detection and for specific and ubiquitous cdetection and identification of an algal, archaeal, bacterial, fungal cc and parasities and using the method of the invention can be used for the universal contection of any bacterium, fungus or parasite in a sample and for the cdetection of any bacterium, fungus or parasite in a sample and for the cleast one toxin gene. hexA nucleic acids are used for the specific and cubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against corroorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp., cc Corynebacteriaceae family, Pseudomonads group, Escherichia coli, colidate in a sample and staphylococcus sp. Using DNA based tests convolved in an hour and improved accuracy is also achieved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids of tuf, fus, atpD and/or recA genes from which pro and/or primers are derived. The method comprises amplifying the acids of determined algal, archaeal, bacterial functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for generating a repertory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                   AAH00010 to
                                          determined in an hour and improved accuracy is also achieved H00010 to AAH002304 represent nucleotide sequences and primers ich are given in the exemplification of the present invention
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                                        given in
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                                             present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a test sample
                                                                 primers/probes
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RESULT 3
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Best Local
Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                            1161
                                                                                                                                                                                                                                                                                                           1916
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                                                                                                                                                                                      AAH01014 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1796
                                                                                                                   24-JUL-2001
                                                                                                                                                     AAH01014;
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                                                                                                                                                                                                                                                                                                          ACGACTACC
                                                                                                                                                                                                                                                                                                                                                                             TCATCATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGT 1915
                                                                                                                                                                                                                                                                                                                                                                                                           gctcgttctacgtggaactcacctgctccacaacaacccccatcaactgaaagttcaagc 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCGTTCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGC 1855
                                                                                                                                                                                                                                                                                                                                             tcatcatcagatagttcaacttcacagtctagctcaaccactccaagcacaaataatagt
                                                                                                                                                                                                                                                                                                                                                                                                                                 129;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                   (first entry)
                                                                                 pneumoniae nucleotide sequence
                                                                                                                                                                                                                                                                                                           1924
                                                                                                                                                                                        DNA;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 Crelated microorganisms e.g. algae, archaea, bacteria, fungi and Comparasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of any bacterium, fungus or parasite in a sample and for the CC least one toxin gene. hexA nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group CC which can be detected include Abiotrophia adiacens, Bordetella sp., CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., CC Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests CC provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                   1799
                                                                                                                                                                                                                            1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
 1919
                                      1104
                                                                                                                1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequences are us primers which can be used to archaeal, bacterial, fungal a
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19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                        Sequence 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                       984
                                                                                                                                                                                                     GATTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCT
                                                      TCATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACG
                                                                                                            cgttctacgtggagctcacctgctccacaaccaacccccatcaactgaaagttcaagctca
                                                                                                                                                 CGTTCTACGTGGAACTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCA
                                                                                                                                                                                    gattggaatataccagaggggctctacagaaatggagaattcgtatttaaaaatggtgct 1043
ACTACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-245006/25
                                  tcatcagatagttcaacttcacagtctaactcaaccactccaagcacaaataatagtacg
                                                                                                                                                                                                                                                                 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Page 961-962; 1580pp; English.
                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences are used to generate universal probes h can be used to identify and detect the presence cterial, fungal and parasitical species in a test
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                                                                                                                                                                                                                                                                                                                                                          BP;
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                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                              6.4%;
99.1%;
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                                                                                                                                                                                                                                                                                Score 127;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                          235
                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                DB 22;
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                                                                                                                                                                                                                                                                                                Length 1212;
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                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                 detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abittrophia addiscens.
                                                                                                                                                                                                                                                                                                                                                               acids of determined algal, archaeal, bacterial, fungal and parasit: species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous
                                                                   which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results be determined in an hour and improved accuracy is also achieved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                   which
                                                       be determined AAH00010 to AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
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19-MAY-2000; 2000CA-2307010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               crids of tuf, fus, atpD and/or recA genes from which probes
primers are derived. The method comprises amplifying the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MG,
                                 to AAH002304 represent nucleote given in the exemplification
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CC rucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic cc acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and cparasites, for universal detection and for specific and ubiquitous certains and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) cobtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium, fungus or parasite in a sample and for the cottent of any bacterium can be used for the specific and cottent on the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of any bacterium fungus or parasite in a sample and for the cottent of the cotte
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Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
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Nucleic acid sequences are used to generate universal probes a primers which can be used to identify and detect the presence
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19-MAY-2000;
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                                                                                    WPI; 2001-245006/25
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                                                                                                                                                                                                                   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                984
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Pred. No. 1.6e-54;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC nucleic acids of tut, fus, atpD and/or recA genes from which probes cand/or primers are derived. The method comprises amplifying the nucleic cacids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and parasitical species and identification of an algal, archaeal, bacterial, fungal and comparasities, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal conditions are used for the universal detection of an algal, archaeal, bacterial, fungal conditions are used for the universal detection of any bacterium, fungus or parasite in a sample and for the conditions of a sample and for the conditions of the sample and for the conditions of at least one antimicrobial agent resistance gene or at constitutions detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., corrected include Abiotrophia adiacens, Bordetella sp., in the condition of its conditions. Escherichia coli:
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Best Local
                                                                                                                                                                                                          microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance;
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                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                vaccine;
                                                                                                                                                                                    catalytic subunit of proton-translocating
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                                                                                                                                                              primer;
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                                                                                                                                                                                                                                                                                                                            pneumoniae nucleotide sequence
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                                                                                                                                                                                                                                              fungal; probe; detection;
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В

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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical Species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC used for producing probes and/or primers for detecting one or more cc related microorganisms e.g. algae, archaea, bacteria, fungal and garasities, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal acc detection of any bacterium, fungus or parasite in a sample and for the contained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cleast one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. CC (1) can be used to design a therapeutic agent which is effective against combined and for identification of streptococcus pneumoniae. CC wynobacterium sp. Enterobacteriaceae group, Escherichia coli, corynebacterium sp. Enterobacteriaceae group, Escherichia coli, corynebacterium sp. Enterobacteriaceae group, Escherichia coli, corynebacterium sp. Enterobacteriaceae group, Escherichia coli, corynebacteriaceae family, Pseudomonads group, Streptococcus sp. Using DNA based tests con be determined in an hour and improved accuracy is also achieved.

CC hallough to AaH00010 to AaH002304 represent nucleotide sequences and primers/probes carious which are result to the accuracy in a few present invention.
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266 C;
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                               ACTACCAATCCTAACAATAATACGCAACAATCAAATACAACCCC
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AAH01018 RESULT В Qy В Qy 멍 Ω Дb

24-JUL-2001

(first entry)

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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpl and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic cc acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal CC detection of any bacteriam, fungus or parasite in a sample and for the CC least one toxin gene. hexA nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., CC Mycobacterium sp., Enterobacteriaceae group, Escherichia coli, CC Mycobacteriaceae and Stabhylococcus sp. Using NAA hased tests
                                                                                                           Matches
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Best Local :
                                                                                                                                                                                                                                                                                                       Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/prowhich are given in the exemplification of the sequences.
                    1842 CTGAAAGTTCAAGCTCATCATCAGATAGTTCAACCTTCACAGTCTAGCTCAACCACTCCAA 1901
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19-MAY-2000;
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     The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic conditions of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be considered microorganisms e.g. algae, archaea, bacteria, fungal and parasitical species with a combination of an algal, archaea, bacteria, fungal and considered microorganisms e.g. algae, archaea, bacteria, fungal and considered microorganisms e.g. algae, archaea, bacteria, fungal and considered microorganisms e.g. algae, archaea, bacteria, fungal and considered using the method of an algal, archaeal, bacterial, fungal conditions of any bacterium, fungus or parasite in a sample and for the considered using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and considered to design a therapeutic agent which is effective against considered to design a therapeutic agent which is effective against considered include Abiotrophia adiacens, Bordetella sp., considered in an appeal and staphylococcus sp. Using DNA based tests considered in an hour and improved accuracy is also achieved.
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nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
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19-MAY-2000;
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algal; archaeal; bacterial; fungal;
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                                                                                                                                                                                                                                              English
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Pred. No.
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. 6.2e-52;
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test sample -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and parasitical species, genus, family and group. A nucleic acid (1) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coll, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria concernace and Strahlylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                       identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1153
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                                                       Nucleic
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae.
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                                                                                                                                                               (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                      28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                            vaccine;
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                                        acid sequences which can be us
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Oy PH;
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                       used to generate universal probes a to identify and detect the presence 1 and parasitical species in a test
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                                                                                                                                  Menard
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Claim 27; Page 1471; 1580pp; English

archaeal, primers

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AAH01019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpb and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group CC Corynebacteriaceae family, Pseudomonads group, Escherichia coll.

CC Mycobacteriaceae family, Pseudomonads group, Escherichia coll.

CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests CC unit of the analysis of the specific can be determined in an hour and improved accuracy is also achieved.

CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species specific; genus specific; family specific; probe; deta identification; algal; archaeal; bacterial; fungal; parasitics microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance;
                                                                                     28-SEP-1999;
19-MAY-2000;
                                                                                                                                                                                28-SEP-2000;
                                                                                                                                                                                                                                               05-APR-2001
                                                                                                                                                                                                                                                                                                             WO200123604-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalytic subunit of proton-translocating ATPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1242 BP;
                      (INFE-) INFECTIO DIAGNOSTIC (IDI) INC
                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 ATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATATTTACAATACAGACGAATACGTTG 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                 99CA-2283458
2000CA-2307010
                                                                                                                                                                                2000WO-CA01150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae nucleotide sequence
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100.0%;
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Pred. No.
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and parasitical species, genus, family and group. A nucleic acid (1) cobtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the universal content of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptcococus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Nycobacteriaceae family, Pseudomonads group, Streptcoccus sp. Weisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.
Matches
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical sending companies and archaeal bacterial and identification of an algal, archaeal, bacterial, fungal and parasitical sending acount a nucleic acid. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequence primers which can be
                                                                                                   Sequence
                                                                                                                                          which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 965; 1580pp; English.
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  160;
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                                                                                                     1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hich can be used to bacterial, fungal a
                                                                                                                                            AAH002304 represent nucleotiven in the exemplification
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences are used to generate universal probes and h can be used to identify and detect the presence of algal, cterial, fungal and parasitical species in a test sample -
                                                                                                     BP;
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                   99.4%;
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                                                                                                 272 C;
0;
                 Score 110;
Pred. No. 3
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  Mismatches
                                                                                                                                                                  nucleotide
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                   3e-46;
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                                       Length 1223;
  Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        1063
                          microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                            AAH02065 standard;
               catalytic subunit
                                                                       Species
                                                                                                   Streptococcus
                                                                                                                                 24-JUL-2001
                                                                                                                                                               AAH02065;
                                                                                                                                                                                                                                                                                                                                                                                                                   1813 CTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCATCATCAGATAGTTC
                                                       identification;
                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                  caataatacgcaacaatcaaatacaacccctgatcaacaaa
                                                                                                                                                                                                                                                                                               CAATAATACGCAACAATCAAATACAACCCCTGATCAACAAA 1973
                                                                                                                                                                                                                                                                                                                                                                                      ctcacctgctccaccaccacccccatcaactgaaagttcaagctcatcatcagatagttc
                                                                                                                                                                                                                                                                                                                           aacttcacagtctaactcaaccactccaagcacaaataatagtacgactaccaatcctaa
                                                                                                                                                                                                                                                                                                                                         AACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGACTACCAATCCTAA
                                                                     specific; genus specific; family specific; probe; detection;
                                                                                                                                (first entry)
                                                                                                   pneumoniae nucleotide sequence SEQ
                                                         algal; archaeal;
             of proton-translocating
                                                                                                                                                                                           DNA; 1225
                                                         bacterial;
               ATPase;
                                                         fungal;
                                                                                                                                                                                                                                                                   1223
                                                                                                    ID NO:2058.
               antimicrobial;
                                                         parasitical,
                                           toxin;
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RESULT 4
AAZ35940
ID AAZ3
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AC AAZ3
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                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungi and CC contained using the method of the invention can be used for the universal CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of any bacterium of indentification of streptococcus pneumoniae. CC (1) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group CC which can be detected include Abiotrophia adiacens, Bordetella sp., CC Mycobacteriaceae family, Pseudomonads group, Escherichia coli, CC Mycobacteriaceae family, Pseudomonads group, Escherichia coli, CC Mycobacteriaceae family, Pseudomonads group, Escherichia coli, CC provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                Matches
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Best Local
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                  AAZ35940
                                                   AAZ35940 standard;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1225
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                                                                                                                                                                            815
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19-MAY-2000;
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                                                                                                                                         61
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                                                                                                                                                         GATGAATTGCAAGTCGCTTCTACCATTGTTGATGTTTCTAACGG
                                                                                                                                       gatgaattgcaagtcgcttctaccattgttgatgtttctaacgg
                                                                                                                                                                                                         gaagctcaaaaacatctgtgggatatttacaatacagacgaatacgttgcctatccagac 60
                                                                                                                                                                                                                                                                                  104;
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                     BP;
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100.0%;
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                                                                                                                                                                                                                                                                                                 Score 104;
Pred. No.
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3.7e-43;
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                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                           A polymerase chain reaction (PCR) assays have been developed for CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC und the pbp1A gene. The products and methods can be used for detecting CC s. pneumoniae, particularly antibiotic-resistant strains. They can be CC used for simultaneously diagnosing pneumococcal meningitis and CC identifying any antibiotic-resistant S. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains resistant CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. CC The assays can be used to detect other pathogens causing meningitis. CC S. pneumoniae with a minimum inhibitory concentration (MIC) of CS. pneumoniae with a minimum inhibitory concentration (MIC) of CC. 25-1 micro g/ml where the PCR products detected are a 1043 bp and CC a 224 bp product. The present sequence represents a Streptococcus CC pneumoniae bpp1A transpeptidase encoding region (TER) isolate nucleotide
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              Matches
                              07-FEB-2000
                                                                                      AAZ35941 standard; DNA; 1260
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Fig 4; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain reaction assays useful for the diagnosis of pneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klugman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SAME-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; identification;
                                                            AAZ35941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-)
                                                                                                                                                                                                   635
                                                                                                                                                                                                                                                              575 GAACAGTATGAGAAAGCAGTCAATACACCAATTACTGATGGACTACAAAGTCTCAAAATCA 634
                                                                                                                                                                   61 gcaagtaattaccctgcttacatggataattacctcaagga
                                                                                                                                                                                                                                 ب
                                                                                                                                                                                    GCAAGTAATTACCCTGCTTACATGGATAATTACCTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-601770/51
                                                                                                                                                                                                                                gaacagtatgagaaagcagtcaatacaccaattactgatgactacaaagtctcaaatca
                                                                                                                                                                                                                                                                                              101;
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                                                                                                                                                                                                                                                                                                                                                                        1260
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                                                                                                                                                                                                                                                                                              Conservative
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                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae; penicillin binding protein; pbp2B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding region; TER; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97ZA-0006886
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                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Du Plessis
                                                                                                                                                                                                                                                                                                                                                                      264 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumococcal meningitis;
                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ssays for detecting Streptococcus pneumonia pneumococcal meningitis
                                                                                                                                                                                                                                                                                           Score 101; DB 20;
Pred. No. 1.3e-41;
0; Mismatches 0;
                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                      258 G;
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                                                                                                                                                                                                                                                                                                                                                                      344 T;
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                                                                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance; diagnosis;
                                                                                                                                                                                                                                                                                                                        Length 1260;
                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide
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Streptococcus pneumoniae pbplA TER isolate c) nucleotide sequence.

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                                                                                                                                                                                         RESULT 47
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting specified particularly antibiotic resistant strains. They can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A; transpeptidase encoding region; TER; antibiotic resistance; diagnosis; detection; identification; pneumococcal meningitis; ss.
Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical;
                                                   Streptococcus pneumoniae nucleotide sequence SEQ ID NO:2050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1260 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. pneumoniae with a minimum inhibitory concentration (MIC) of 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbplA transpeptidase encoding region (TER) isolate nucleons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be adapted to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used for simultaneously diagnosing pneumococcal meningitis and identifying any antibiotic-resistant S. pneumoniae strains in a sample The methods can be used for detecting S. pneumoniae strains resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase chain reaction assays for detecting Streptococcus pneumonia useful for the diagnosis of pneumococcal meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-601770/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SAME-) SOUTH AFRICAN INST MEDICAL RES.
(UYWI-) UNIV WITWATERSRAND.
(MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1997;
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                                                                                      24-JUL-2001
                                                                                                                                                        AAH02057 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1999
                                                                                                                                                                                                                                                                            635
                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                       gcaagtaattaccctgcttacatggataattacctcaagga 101
                                                                                                                                                                                                                                                                           GCAAGTAATTACCCTGCTTACATGGATAATTACCTCAAGGA 675
                                                                                                                                                                                                                                                                                                         gaacagtatgagaaagcagtcaatacaccaattactgatggactacaaagtctcaaatca 60
                                                                                                                                                                                                                                                                                                                                            GAACAGTATGAGAAAGCAGTCAATACACCAATTACTGATGGACTACAAAGTCTCAAATCA 634
                                                                                                                                                                                                                                                                                                                                                                              101;
                                                                                                                                                                                                                                                           11; Fig 4; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97ZA-0006886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 A;
                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                               5.1%;
100.0%;
                                                                                                                                                        930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Du Plessis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 C;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 20
Pred. No. 1.3e-4
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 T;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 1260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolate nucleotide
                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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밁 Ş В δÃ

899

CCGACATGATGAAAACAGTCTTGACTTATGGAACTGG 1473

704

1437

Query Match Best Local S Matches 97

. Similarity 97; Conser

Conservative

0;

Mismatches

0;

Gaps

0;

4.9%;

Score 97; Pred. No.

DB 22, 3. 1.5e-39; 3. 0;

Length 930;

1377

608

aaaaaagagttctctaatgtcggaactcgtgccatgaaggaaacgacagcctatatgatga AAAAAGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGA 1436

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The present invention describes a method for generating a repertory of conucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasites, for universal detection and algal, archaeal, bacterial, fungal detection and identification of an algal, archaeal, bacterial, fungal detection of any bacterium, fungus or parasite in a sample and for the obtained using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one antimicrobial agent resistance gene or at least one toxin gene. hexh nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corvenbacterium en Esterotropia agent resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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                                                                                                                                                                                                      Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results
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    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 1466; 1580pp; English.
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19-MAY-2000; 2000CA-2307010
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                                                                               AAH00010 to AAH002304 represent nucleotide sequences and which are given in the exemplification of the present inv
                                                                                                                                                                                                                                                                                                                                      Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergeron MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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                                                                                                                                                              determined in an hour and improved accuracy is also achieved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-245006/25
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    930
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    BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PH;
282 A;
195 C;
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192 G;
    261 T; 0
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    other;
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                                                                                                                           primers/probes
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                                                                  RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                       used for simultaneously diagnosing pneumococcal meningitis and identifying any antibiotic-resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, perferably penicillin. The assays can be adapted to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of
   AAH02071;
                                                                                                                                                                                                   1377 AAAAAGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGA 1436
                                                                                                                                                                                                                                                                                                                                                             0.25-1 micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbplA transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting speciments, particularly antibiotic-resistant strains. They can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; penicillin binding protein; pbp2B; transpeptidase encoding region; TER; antibiotic resistance; detection; identification; pneumococcal meningitis; ss.
                                   AAH02071 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 4; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase chain reaction assays for detecting Streptococcus useful for the diagnosis of pneumococcal meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-601770/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAME-) SOUTH AFRICAN INST MEDICAL RES. (UYWI-) UNIV WITWATERSRAND. (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                  Sequence 1260 BP; 404 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1999
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                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                  CCGACATGATGAAAACAGTCTTGACTTATGGAACTGG
                                                                                                                                                                                aaaaagagttctctaatgtcggaactcgtgccatgaaggaaacgacagcctatatgatga 862
                                                                                                                 ccgacatgatgaaaacagtcttgacttatggaactgg
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith AM,
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                                                                                                                                                                                                                                                                                                                                266 C;
                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                  Score 97;
                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                254 G;
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The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpp and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic conclusion of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more cused for producing probes and/or primers for detecting one or more cused for universal detection and for specific and ubiquitous cused for universal detection and for specific and ubiquitous cused for universal detection and for specific and ubiquitous cused for the species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at cleast one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., conversed tests against general agency agenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocation areas.
                                                                                 Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; Page 1476; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-245006/25
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19-MAY-2000;
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bacterial; fungal
G;
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Qy Db

ATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTATCGTT 1024 atcacagactatgctcctgccttggagtacggtgtctacgattcaactgctactatcgtt

Matches

Local

90; Conser

Conservative

100.0%; 4.5%;

Score 90; DB; Pred. No. 6.2

DB 24, J. 6.2e-36; O;

Length 782;

Indels

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Gaps

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1025 CACGATGAGCCCTATAACTACCCTGGGACA 1054

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The present invention describes a method for generating a repertory of CC nuclaic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical Species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and parasitical species, genus, family and group. A nucleic acid (I) cand parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cettion of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and CC (I) can be used to design a therapeutic agent which is effective against CC (I) can be detected include Abiotrophia adiacens, Bordetella sp., CC (Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., CC (Nycobacteriaceae family, Pseudomonads group, Streptococcus sp., CC (Nycobacteriaceae family, Pseudomonads group, Streptococcus sp., CC (Pseudomonads group), Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 1255; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1999; 99CA-2283458.
19-MAY-2000; 2000CA-2307010.
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Picard FJ,
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                                                                            be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers
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                                                    'n
                                                 the
                                                 exemplification
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                                              nucleotide sequences and primers ication of the present invention
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bacterial; fungal; parasitical;
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                                                                       primers/probes
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Sequence

253 A; 186 C;

164 G;

210 T; 0 other;

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                                                                                                             Matches
                                                                                                                      Query Match
Best Local Similarity
                           1025
                                                    169
                                                                   965 ATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACCTATCGTT 1024
229 cacgatgagccctataactaccctgggaca 258
                           CACGATGAGCCCTATAACTACCCTGGGACA 1054
                                                   atcacagactatgctcctgccttggagtacggtgtctacgattcaactgctactatcgtt 228
                                                                                                           4.5%; So llarity 100.0%; E Conservative 0;
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Pred. No.
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BB
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Search completed: June 13, Job time: 6595 sec 2002, 12:42:27

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 60.0 , Gapext 60.0
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em_htc:*
gb_est1:*
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gb_htc:*
gb_htc:*
em_gss_hum:*
em_gss_pln:*
em_gss_pri:*
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Copyright (c) 1993 - 2000 Compugen
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BG334672 602460969
AQ701777 HS_2134_A
ALZ29519 Tetraodon
AL632585 AL632585
AL397462 fb18b08.x
AL629478 AL629478
AL406462 T3 end of
AL406949 T7 end of
BF174868 MYE3951 M
AA317576 EST19524
BB551207 BB551207
BF016981 ux19c08.y
BF016981 ux19c08.y
BF016982 ux19c08.y
BM173589 900943 Av
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                                                   Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BE852054 uw13h11.x
AQ706156 HS_550_A
AQ307366 HS_550_E
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BJ159565 BJ155965
BJ15966 LERFD25FF
AQ890384 HS_2204_A
BE186915 946014E10
AQ960366 LERFD25FF
AI935410 wo84b10.x
BE599172 P11_46_G1
BH424798 BOHIT12TF
AU200409 AU200409
AQ974457 RPC1-23-3
BJ124261 BJ124261
BH5589050 194786 BA
BF491545 AT281312
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AQ772409 HS_5454_A
AI492144 t912f01.x
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AQ385478 RPCI11-14
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AW632737 92849 MAR
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2:4577753 5',
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                                                                                                                                                                                                                                                                                                                            401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2134 row: E column: 24
Seq primer: M13 Reverse
1.1%;
L Similarity 100.0%;
22; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 553)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ701777 553 bp DNA linear GSS 07-JUL-1999 HS_2134_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2134 Col=24 Row=E, DNA sequence. AQ701777 AQ701777.1 GI:5411203
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University of Washington
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                                                                                                          /note="Organ: sperm;
E-Coli DH10B"
97 c 105 g
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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/db_xref="taxon:9606"
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                                                                                           AL632585 XGC-gastrula Silurana
mRNA sequence
AL632585
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                      western clawed frog.
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/db_xref="taxon:99883"
/clone="215123"
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Email: zbrafish@watson.wustl.edu
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., J., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Und., K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, Swaller, Schurk,R., Ritter, Swaller, Swaller, Schurk,R., Ritter, Swaller, Swaller, Schurk,R., Ritter, Swaller, Swal
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422 bp HKNA THICKLE COUNTY COUNTY CHAIN CHAIN
                                                                                                                                                                                                            Tel: 314 286 1800 Fax: 314 286 1810
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Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: TGas021e05.spd
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Sanger Centre
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                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Contact: Stephen L. Johnson
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/lab_host="Escherichia coli XL1-blue"
/note="Yector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
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/db_xref="taxon:8364"
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Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sander Xenopus tropicalis EST project 2001 (10_2001)
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Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SEQUENCE_ID: TGas018i04.sp6
                              Hinxton, Cambridgeshire, Email: trop@sanger.ac.uk
                                                                           Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                   Silurana tropicalis
                                                                                                                                                                                                                     western clawed frog.
                                                                                                                                                                                                                                                                                  mRNA
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                                                              Sanger Centre
                                                                                                                                                                                                                                                   AL629478.1
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                                                                                                                                                       Kenopodinae; Silurana.
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strand cDNA was primed with a Not I - oligo(dT)15 primer
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/clone="IMAGE:3712215"
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FGas018i04 5',
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                  Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefigenoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 1025)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montign, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
de-Montign, J., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies
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FEBS Lett. 487 (1), 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F., Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
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                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                     Genoscope.
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keywords for
                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 487
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/lab_host="Sscherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: ECCRI; Site_2: NotI; cDN/
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
ind pCS107 with EcoRI at the 5' end and NotI at the 3'
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/clone_lib="XGC-gastrula"
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/db_xref="taxon:8364"
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  description of this sequence and for the sequence of
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Pred. No.
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                                                                                                        Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr) www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces Servazii, Zygosaccharomyces rouxil, Saccharomyces Servazii, Zygosaccharomyces rouxil, Saccharomyces Kluyveromyces harmotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Caratis, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Caratis, Debaryomyces hansenii var.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Souciet, J.L., Aigle, M., Artiquenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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1 (bases 1 to 1078)

Neuveglise, C., Bon, E., Lepingle, A., Wincker, P., Artiguenave, F., Gaillardin, C. and Casaregola, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Saccharomyces kluyveri, genomic survey sequence. AL406949
AL406949.1 GI:12171649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS06NM7 1078 bp DNA linear GSS 04-JUL-20
T7 end of clone AUOAAO15C12 of library AUOAA from strain CBS 3082
                 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Location/Qualifiers
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/evidence=not_experimental
191 c 205 g 280 t
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/strain="CBS 3082"
/db_xref="taxon:4934"
/clone="AU0AA010D02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="AUOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extremity of this insert. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%;
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Pred. No.
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14;
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inhibitor ]"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610 University Ave.,
Tel: (416) 946-4639
Fax: (416) 946-6546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: 5'-GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3'
BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seq primer: 5'-GAAATTAACCCTCACTAAAGG-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: A. Keith Stewart, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Franciso-Pabalan, O., Liew, C.C. and Stewart, A.K. The transcriptional phenotype of myeloma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claudio, J.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/Cell_type="myeloma"
/dev_stage="multiple myeloma"
/dev_stage="multiple myeloma"
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: Lambda Zap Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: Lambda Zap Express; Site_1: Lambda Zap Express;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         k.stewart@utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<1. .>1074)
/note="similar to Saccharomyces cerevisiae ORF YGR233c [
PHO81; cyclin-dependent kinase inhibitor ]"
/evidence=not_experimental
1 218 c 214 g 345 t 1 others
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/db_xref="taxon:4934"
/clone="AUOAA015C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Myeloma (MYE) cDNA library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell_type="myeloma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang,H., Khan,E.M., Voralia,M., Li,Z., lan,O., Liew,C.C. and Stewart,A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237)
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Pred. No.
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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VERSION
KEYWORDS
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                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M., Shirley, R., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA317576 287 bp EST19524 Retina II Homo sapiens protein PO-GA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: THC171722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96026280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 287)
                                                                                                                                                         primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research
Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 a
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                      /organism="Homo sapiens"
/db_xref="ATCC (inhost):118036"
/db_xref="taxon:9606"
                                                                                                                             Location/Qualifiers
/clone_lib="Retina II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%;
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Pred. No.
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JOURNAL COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Konno, H. Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kal, C., Kawal, J., Kikuchi, N., Kiyosawa, H., Kojina, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, T., Mixin, Y., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB551207 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230026H21 3' similar to D10712 Mus musculus mRNA for nedd-1 protein, mRNA sequence.

BB551207
                                                                                                                                                                                            Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yano,R., Yasunishi,A., Yokota,T., Yoshida,K.,
,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 295)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                        Y. and Hayashizaki,Y.
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                                                                                                                                           visit our web
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/note="Organ: retnina; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: xhoI"
57 c 64 g 52 t 1 others
/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                     Location/Qualifiers
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                                                                                                                                        site (http://genome.rtc.riken.go.jp) for
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Query Match
Best Local
                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF016990 360 bp mRNA linear EST 10-OCT-20 ux19d08.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3471951 5' similar to SW:NED1_MOUSE P33215 NEDD1 PROTEIN ;,
                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 360)
                                                                                                                                                                                                                                   High quality sequence stop: 3
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF016990
                                                                                                                                                                                                                                                                                              MGI:1391311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence
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                                                                                                                                                                                                                                                                             primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dT) primer (5')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 86 c 53 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:3471951"
/clone_1ib="Soares_thymus_2NbMT"
                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult female oviduct"
/sex="female"
                                                                                                             /sex="male"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 days pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 10-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 1 BF016990

DEFINITION

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Matches

BASE COUNT

FEATURES

Query Match Best Local Similarity

1.0%;

Score :

20; . No. 38;

10;

Length 367

COMMENT

JOURNAL

REFERENCE

TITLE AUTHORS VERSION KEYWORDS

ACCESSION

SOURCE

ORGANISM

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RESULT 13
BF016981
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ORIGIN
           BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 AACCAAGCAAGAATCTTGA 251
                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Other_ESTs: ux19c08.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF016981 367 bp mRNA linear EST 10-OCT-20 ux19c08.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3471950 5' similar to SW:NED1_MOUSE P33215 NEDD1 PROTEIN ;,
                                                                                                                                                                                                                                                                                                              High quality sequence stop:
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse
             114
                                                                                                                                                                                                                                                                                                                                           primer: -40RP from Gibco
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        /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:3471950"
                                                                                                                                                                                                                                                                     /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                           /clone_lib="Soares_thymus_2NbMT"
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38;
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EST 10-OCT-2000

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BM173589
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TITLE
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  1281 GTGAAAAGATGGCTGCT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AACCAAGCAAGAATCTTGA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Avicenniaceae; Avicennia.

1 (bases 1 to 402)
Parani, M., Mehta, P., Sivaprakash, K.R. and Parida, A.
Expressed sequence tags from the mangrove species Avicennia marina Unpublished (2000)
Contact: Parani M / Parida A
Department of Plant Molecular Biology
M. S. Swaminathan Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM173589

402 bp mRNA linear EST 04-DEC-2001 900943 Avicennia marina leaf cDNA Library Avicennia marina cDNA clone Am900943 5' similar to NADH dehydrogenase subunit 5 (AF085145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on November 6th 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLAST search in BLASTX (Non-redundant)using default parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 91-44-2351319
Fax: 91-44-2351319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avicennia marina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM173589.1 GI:17313152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mangrovegenes@mssrf.res.in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avicennia marina.
                                                               Similarity
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                                          Conservative
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                                                                                                                                                                                               /note="A one year-old plant from the natural mangrove habitat in Pichavaram, Tamil Nadu, India was collected and brought to the M.S.Swaminatan Research Foundation. The whole plant was treated with the nutrient solution supplemented with 500 mM NaCl for 48 hours, Poly(A+)mRNA from the leaf tissue was purified and cDNA was prepared using Superscript Lambda System (Life Technologies, Cat. No. 19643-014). The cDNAs were size fractionated over SizeSep-400 spun column (Amersham-Pharmacia Biotech Cat No. 27-5105-01) and cloned in 5/Sal I - 3/Not I of pspORT1 (Life Technologies Cat. No. 15383-011). The ESTs were sequenced from the 5' end using M13/pUCl8 reverse primer in an Automated Sequencer (ABI310, Applied Biosystems) and submitted after editing to remove the vector and adapter sequences. BLAST search in BLASTX (Non-redundant)was carried out on 7th August, 2000 using default parameters and the results reported under
                                                                                                                                                                                    putative identification/comment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Avicennia marina"
/strain="Pichavaram"
/db_xref="taxon:82927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Avicennia marina leaf cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Am900943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="1 year old plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Hermaphrodite"
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                                                             DB 10;
39;
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                                                                             Length 402;
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                                                                                                                                                                                                                          283 AACCAAGCAAGAAATCTTGA 302
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                                                                     AQ445724 406 bp
nbxb0054407f CUGI Rice BAC Library
nbxb0054J07f, DNA sequence.
                     AQ445724
AQ445724.2 GI:6582598
GSS.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1391312
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Oryza sativa
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 344.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              provided by Dr. Bertrand Jordan. Library went through rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

101 c 88 g 92 t
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/dev_stage="4 weeks"
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/clone="IMAGE:3471952"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_thymus_2NbMT"
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                                                                                                                                                                                                                                                                                                                           1.0%;
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                                                                                                                                                                                                                                                                                                                           Score 20; DB Pred. No. 39;
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                                                                                                             VERSION
                                                                                                                                ACCESSION
                                                                                                                                                                                                                 BG017796
                                                                                                                                                                                                                                   RESULT 17
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Best Local
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                                                                                                                                                                                                                                                                                                                        636 CAAGTAATTACCCTGCTTAC 655
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                                                                                                                              BG017796

440 bp mRNA linear EST 30-JAN-200 dab10fil.yl NICHD XGC Sp1 Xenopus laevis cDNA clone IMAGE:4174220 5' similar to TR:Q9QYI6 Q9QYI6 MDJ7.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
On Dec 15, 1999 this sequence version replaced gi:4574947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzeae; Oryza.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                             Xenopus laevis
                                                               African clawed frog.
                                                                                                        BG017796.1 GI:12472380
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="nbxb0054J07f"
/clone_llb="CUGI Rice BAC Library"
/tlssue_type=""ueaf"
/lab_bost="E. coli DH10B"
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39;
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Matches 20; Conserv
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1306 TGCCTTTGCAAATGGTGGAA 1325
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                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                           Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakazime,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB824552 RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA Mus musculus cDNA clone G830033I20 3', mRNA
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Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                       RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB824552.1 GI:17002795
Email: genome-res@gsc.riken.go.jp,
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/note="Organ: spleen; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Olig
Average insert size 2.4 kb. Constructed by Life
Technologies."

3 c 99 g 122 t
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/db_xref="taxon:8355"
/clone="IMAGE:4174220"
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/dev_stage="adult"
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RESULT 1
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JOURNAL
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                                            High quality sequence stop: 441.
Location/Qualifiers
                                                                                        CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM365 row: g column: 22
                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishkawa, T., Ozawa, Y., Tanka, T., Matsuura
                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE566388.1 GI:9810108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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/tissue_type="mammary gland"
/cell_line="RCB-0526 Jyg-MC(A)"
93 c 109 g 102 t
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/organism="Homo sapiens"
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National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Jeffery L. Miller
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il: jm7f@nih.gov
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/lisble_type="carcinoma, cell line"
/lab_host="pH10B (Tl phage-resistant)"
/note="Organ: bladder; Vector: pDNr-LIB (Clontech);
/note="Organ: bladder; Vector: bladder; 
                                                                                           /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                        /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Proliferating Human Erythroid Cells (LCB:ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ax28e04"
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Drgan: blood; Vector: Lambda ZAP II; Site_1:
ECORI; 65,000 proliferating erythroid cells
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuu, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Inotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-Length cDNAs (Akimura, T., et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
                              sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
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                                                                                                                                     Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                               RIKEN integrated sequence analysis (RISA) system -- 384 - format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIZOl reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder CDNA Library Construction Kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Clontech) according to the manufacturer's protocol and
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Pred. No.
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   Shibata, K.,
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40;
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Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                             sequencer. Genome
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REFERENCE AUTHORS

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION

COMMENT

JOURNAL TITLE BB750480

DEFINITION

밁

Matches

ORIGIN BASE COUNT

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KEYWORDS
SOURCE
ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
AA280963
AA280963.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA280963 493 bp mRNA linear EST 15-AUG-1997 zs97d12.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711575 5' similar to gb:L23320 ACTIVATOR 1 140 KD SUBUNIT (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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a 94
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pt7T3D-Pac (Pharmacia) with a modified
/note="Vector: pt7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Alland
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
                                                                                                                                                                                                                                                                                                                             1. .493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebellum, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G130003N12"
                                                                                                                                                                                                                          /clone="IMAGE:711575"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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cerebellum etc"
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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dev_stage=16 days neonate, sex=mixed),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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100.0%;
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Pred. No.
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                                                     David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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AW762116
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TITLE
Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Other_ESTs: ur53h07.xl
Other_ESTs: ur53h07.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINIA at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW762116
ur53h07.yl NCI_CGAP_Mam3 Mus mus
similar to gb:D10712 Mouse mRNA
(MOUSE);, mRNA sequence.
AW762116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 405
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1056801
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20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 526)
                                                                                                          159
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                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-xia Deng, NH Reference for transgenic model: Xu et al., Nature Genetic: 22, 37-43 (1999)."
                                                                                                                                                                                                                                  /dev_stage="10 months"
/lab_host="DH10B"
/nofe="^~~~

    Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was

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94 c 115 g 96 t
                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross
                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="129 - C57/B6 -
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:3154045"
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Pred. No.
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                      Length 526;
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AZ824983 535 bp DNA linear GSS 20-FEB-200 2M0099724R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic clone
AQ710693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darilability, please contact Pleter de Jong
Library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
High quality sequence stop: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.htsc.washington.edu
Plate: 920 row: I column: 20
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University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahairas,G.G., Wallace
Keller,A., Shaker,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 526)
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GSS.
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                                                                                                                                                                                                                                                                                                             /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

103 c 113 g 185 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=920 Col=20 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                   100.0%;
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Pred. No.
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Adams,M.D.
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                         20-FEB-2001
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                                                                                            AACCAAGCAAGAAATCTTGA 320
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University of Utah Genome Center
University of Utah
BG723460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: J column: 24
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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AZ824983
                                                                                                                                                                       Similarity 100.
20; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWA2 (gil4732114|gb)AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                        purified. The sheared, adaptored mouse DNA was anneased to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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/clone="UUGC2M0099J24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                              1.0%;
                                                                                                                                                                                                                                                                                                                                                               The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                       0;
                                                                                                                                                                                       Score 20;
Pred. No.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 587)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG503218
BG503218.1 GI:13464735
EST.
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1 (bases 1 to 563)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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BG723460.1 GI:14002647
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4826218"
/clone_ib="NHM_MGC_97"
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E:4658644 5',
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                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602567826F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692414
                                                                                                                                              http://image.llnl.gov
Plate: LLCM1513 row: c column: 07
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLCM1453 row: d column:
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Location/Qualifiers
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgctctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0)-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
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/clone="IMAGE:4658644"
/clone_lib="NIH_MGC_61"
/clone="IMAGE:4692414"
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
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Location/Qualifiers
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314 286 1810
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_l:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_l:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGGCGGACTAGTGGT-3') BN-3' (Where B = A,
C, Or G and N = A, C, G, Or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by GR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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/clone="IMAGE:1005949"
/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="B6D2 F1/J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                           /lab_host="DH10B"
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Pred. No.
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Best Local
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Best Local Similarity
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                                                         319 AAAAGCAACCAAGCAAGAAA 338
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                               AAAAGCAACCAAGCAAGAAA 293
                                                                                                                                  20; Conser
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High quality sequence stop: 649.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 650)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG492386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                   258
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                                                                                                                            1.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                /tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/fil (ggccgctctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGGCGAATTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGATTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratorles (Palo Alto, CA). Note: this is a NIH_MGC
ribrary "10 colories (Palo Alto, CA). Note: this is a NIH_MGC
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138 c 143
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/clone="IMAGE:4655307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Primates;
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Pred. No.
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Pred. No.
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                                                                                                                                                      DB 10;
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43;
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LOCUS
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Hayashizaki,Y.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 661)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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BB498524 RIKEN full-length enriched, 0 day neonate kidney Mus
musculus cDNA clone D630015B03 3', mRNA sequence.
BB498524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                   CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                            prepare
                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jul 26, 2000 this sequence version replaced gi:9473625 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
On Jul 26, 2000 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA
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                          /tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                     kidney'
                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D630015B03"
                                                                                                                                                                                                                                                  Location/Qualifiers
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                            /clone_lib="RIKEN full-length enriched,
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High quality sequence stop: 633
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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/clone_lib="NIH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
/note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
/note="Organ: bone marrow; Vector: pD
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/db_xref="taxon:9606"
/clone="IMAGE:4047787"
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mg56C03.rl Soares_thymus_2NbMT Mus
5' similar to gb:D10712 Mouse mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthritis Cartilage 9 (7), 641-653 (2001)
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 610-270-7245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sanjay Kumar
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                                       (MOUSE);, mRNA sequence
                                                                                                                                                                                                              Similarity 100
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: sanjay_kumar-1@gsk.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 709 Swedeland Road,
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/lab_host="E.coli DH10 B"
/note="Vector: psport I; Site_1:
//soction:
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/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
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                                                    musculus cDNA clone for nedd-1 protein,
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Homo sapiens cDNA
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                                                                                                                                                                               BF658632 710 bp mRNA linear EST 20-DEC-20 maa98h01.yl Soares_thymus_2NbMT Mus musculus cDNA clone maa98h01.yl Soares_thymus_2NbMT Mus musculus cDNA clone maa98h01.yl Soares_thymus_2NbMT Mus musculus cDNA clone maa98h01.yl Soares_thymus_2NbMT Musculus cDNA clone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 710)
                                                                         Mus musculus
                                                                                                                              BF658632.1
                                                                                                                                                 BF658632
                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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163 c 171 g 154 t 2 others
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:582724"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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                                     Murinae;
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattorı, m. Totoki, Y., Watanabe, H.
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama, A., Hattori, M.,
Totoki, Y., Watanabe, H. a
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Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/clone="IMAGE:3824881"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                        ., Toyoda, A., Taylor, T.D., Yada, T., and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Toyoda, A., and Sakaki, Y.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 CCTTGCTGGCTGGAATGCCT 472
                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: L/LM916 row: 1 column: 18
High quality sequence stop: 712.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 731)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           namur
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R.Site 2
           /clone_lib="NIH_MGC_77"
//lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontes: 5' adaptor sequence: 5'-CACGGCCAFTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCAFTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACTATGG-dT(30)BN-3' (where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.9
/c or G and N = A, C, G, Or T). Average insert size 1.9
/kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by Crantech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4071257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
200 c 158 g 192 t
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/db_xref="taxon:9598"
/clone="PTB-102807.F"
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Pred. No.
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44;
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5 others
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VERSION
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AZ354492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0093 row: I column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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1 (bases 1 to 737)
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1M0093I15R Mouse 10kb plasmid UUGC1M library
clone UUGC1M0093I15 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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      231
                                                                                                         musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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         Q
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

178 c 146 g 181 t 1 others
                                                                                           purified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0093I15"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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                                                                                         The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 9
High quality sequence stop: 528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                             /db_xrel="taxou:yvvv
/clone="IMAGE:4134678"
/clone_lib="NIH_MGC_54"
/clone_lib="NIH_MGC_54"
/clone_lib="NIH_MGC_54"
/clone_lib="NIH_MGC_54"
/tlssue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_l: SfiI (ggcgctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5; and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         41
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BI690754
                                                                                                                                                                                                                                                                                                                                                                          BI690754 803 bp mRNA linear 603314371F1 NCI_CGAP_Mam6 Mus musculus cDNA clone
                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                          Mammalia; Eutheria; Rodentia; 1 (bases 1 to 803)
VIH-MGC http://w-
                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa;
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BE889059
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http://image.llnl.gov
Platte: LLAM9738 row: i column: 24
High quality sequence stop: 716.
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                                                                                                                                                                                                                                                                              house mouse
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Clone distribution: MGC clone distribution information can be
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3915399"
/clone_lib="NHH_MGC_71"
/fissue_type="leiomyosarcoma"
/lab_host="DHHOB (phage-resistant)"
/note="organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 138 c 182 g 157 t
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Sciurognathi;
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 788;
                                                                                                                                                          Gene Collection (MGC)
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IMAGE:5354320 5',
                                                                                                                                                                                                                   Euteleostomi;
Murinae; Mus
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BF667800
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1105 row: g column: 06
High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov,
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF667800 841 bp mRNA linear EST 21-DI 602122620F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4279709
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Plate: LLAM11900 row: n column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: CLONETECH Laboratories, I CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/organism="Homo sapiens"
/organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:4279709"
/clone="IMAGE:42797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" a 174 c 182 g 195 t
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/clone="IMAGE:5354320"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tssue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/strain="FVB/N"
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Pred. No.
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Mismatches
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KEYWORDS
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Best Local
                                                                                       Matches
                                                                                                                                              Query Match
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74 GATATTCCCACAGATTTGGT 93
                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                       . Similarity
20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM313 row: m column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 68 High quality sequence stop: 558.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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601298315F1 NIH_MGC_19 Homo sapiens
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                                                                                 1.0%; S. larity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                /clone_"IMAGE: 5628587"
/clone_lib="NNH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="NH10B (phage-resistant)

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136 c 220 g 160 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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Tel: 301-838-3523
Fax: 301-838-0208
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                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF670847.1 GI:11944742
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National Institutes of Health, Mammalian
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20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 a
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/clone_lib="NMH_MGC_81"
/clone_lib="NMH_MGC_81"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="Director to the content of the cloning of the c
/clone="IMAGE:4282542"
/clone_lib="NIH_MGC_56"
/tissue_type="prinitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
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                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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BASE COUNT
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AUTHORS
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ORGANISM
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VERSION
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BF247101
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ORIGIN
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Query Match
Best Local Similarity
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Best Local :
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http://image.llnl.gov
Plate: LLCM924 row: h column: 11
High quality sequence stop: 556.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4074298"
/clone=Lib="NHH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (TI phage-resistant)"
/hote="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-CACGGCCATGGCCCGCACATG-dT(30)BN-3'
(Where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGCGAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA) "
2 others
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Pred. No.
Score 20;
Pred. No.
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. 47;
  DB 10;
47;
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                     Length 904;
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RESULT 49
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mRNA sequence.
BG282996
BG282996.1 GI:13032433
                                                                      BG282996 938 bp mRNA linear EST 21-FEB-2001 602406185F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4518260 5',
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BF697265
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1123 row: i column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_ilb="NAGE_56"
/clone_ilb="NAH_MGC_56"
/clone_ilb="NHH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH1DB (TI phage-resistant)"
// Still (ggccgcttggcc); Site_1: ggccattataggcc);
Still (ggccgcctattaggcc); Site_1: ggccattataggcc);
Still (ggccgcctattaggcc); Site_1: ggccattataggcc);
Still (ggccgcctattaggcc); Site_1: ggccattataggcc);
Adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCAATGATGCGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCAATGATGC-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This:library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

43 a 187 c 229 g 158 t
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                    1 (bases 1 to 969)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear GSS 01-JUL-1999 nbxb0077M07r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0077M07r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                      100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                   Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
                       Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                    Contact: Wing RA
                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ688268
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Plate: LLAM10412 row: j column:
High quality sequence stop: 719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ688268.1 GI:5329352
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High quality sequence stop: 338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/db_xref="taxon:9606"
/clone="IMAGE:4518260"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
90 a 152 c 175 g 321 t
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                   //lab_host="E. coli DH10B"
//lab_host="E. coli D
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/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
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/db_xref="taxon:4530"
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Matches Query Match Best Local : 636 CAAGTAATTACCCTGCTTAC 655 Local Similarity Conservative 1.0%; 0, Score 20; Pred. No. Mismatches DB 12; 48; 0; Length 969; Indels 0 Gaps

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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-08-961-083-228

US-08-961-083-228

US-09-103-657-5

US-09-020-956-5

US-09-030-607-5

US-09-444-053-3

US-09-444-053-3

US-09-444-053-3

US-09-444-053-3

US-09-444-17

US-08-630-0144-2

US-08-630-02-17

US-08-637-080-65

US-08-637-080-65

US-08-687-080-65

US-08-687-080-65

US-08-688-207A-116

US-08-858-207A-116

US-08-858-207A-116

US-08-858-207A-31

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US-08-961-083-1
; Sequence 1, Application
; Patent No. 6159469
; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 983,473
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8514
TELEPAX: (301) 309-8514
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
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ADDRESSEE: Human Gen
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STATE: Maryland
COUNTRY: USA
ZIP: 20850
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Best Local Similarity 100.0%;
Matches 1999; Conservative 0
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LENGTH: 1999 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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               TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
                                                                                   AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT
                                                                                                                                                      ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA
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                                                                                                Query Match 71.9%;
Best Local Similarity 99.4%;
Matches 1988; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IN 580
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,4:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                 LOCATION: FEATURE:
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                                                                                                                                                                                                                                                                      STRAIN: PM 1
IMMEDIATE SOURCE:
LIBRARY: PCR cloning
CLONE: PARC 0512 Sol
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                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
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RESULT 3
US-08-245-511-3
US-08-245-511-3
Sequence 3, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
FITLE OF INVENTION: BACTERTAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack

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Best Local S
Matches 946
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
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CLONE: SPRU42
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                              Local Similarity
nes 946; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                     TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA
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99.7%;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08600993A Patent No. 5981229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                           CURRENT ARTELECTION NUMBER: US/08
APPLICATION NUMBER: US/08
FILING DATE: 1-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 59
                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541
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CITY: Hackensack
STATE: New Jerse
                                                CLASSIFICATION:
                                                               FILING DATE:
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600

26,742 ER: 600-1-069

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Best Local :
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LENGTH: 960 base pairs
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TELEFAX: 133521
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LOCATION:
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0; Mismatches
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                            Matches
                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Choi et.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                              TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   KEGLSTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: HP Vectra 486
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: Human Gen
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CITY: Rockville
STATE: Maryland
                                                                                                             TOPOLOGY:
                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                   NAME:
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                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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 1 TAAAATCTACGACAATAAAAATC
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9410 Key
                                                                                                                                                    33 base pairs
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                            Conservative
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HP Vectra 486/33
eversion 6 2
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West Avenue
                                         100.0%;
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Streptococcus pneumoniae
452
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                                         Score 23; DB 3; Pred. No. 0.033;
  23
                             Mismatches
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US-08-731-716-1
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                                                                   Sequence 3, Application US/08731716
Patent No. 5789202
GENERAL INFORMATION:
                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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                                        APPLICANT:
                                                                                                                                                                                        1301 TACGCTGCCTTTGCAAATG 1319
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
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APPLICANT:
                                                                                                                                                                      1555 TACGCTGCCTTTGCAAATG 1573
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2193 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: No. 5789202ris, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein From
TITLE OF INVENTION: Streptococcus Pneumoniae
APPLICANT:
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                            APPLICANT:
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CITY: I
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                                                                                                                                                                                                                               19;
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5789202
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Y: U.S.
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          Zhao,
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Rockey, Pamela K.
           Rockey, Pamela K.
Zhao, Genshi
                                        Hoskins, JoAnn
Jaskunas, S. Richard
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                                                                                                                                                                                                                                            Score 19;
Pred. No.
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; ORGANISM: Homo sapiens US-09-103-875-2
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                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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Best Local Similarity 68.4
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                        TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE FILE OF INVENTION: OLIGONUCLEOTIDES FILE REFERENCE: 106101.194
CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT FILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: 60/069,865
EARLIER APPLICATION NUMBER: 60/069,865
EARLIER FILING DATE: 1997-12-17
EARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                            APPLICANT: Szyf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
                                                                                                            NUMBER OF SEQ ID NOS: 138
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                                TYPE: DNA
                                                  LENGTH:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
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HYPOTHETICAL:
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LENGTH: 2193 base pairs
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5. 6221849
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RESULT 10
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                                                                                                               Sequence 5, Application US/09020956 Patent No. 6261562
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                     Query Match
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                                                     GENERAL INFORMATION:
APPLICANT: Xu, Jian
APPLICANT: Dillin,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                               1983 CTCAACCAGCACAACCA 1999
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LENGTH: '27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VES
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
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              ADDRESSEE:
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6300 Columbia Center,
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                                                                                                                                                                                                                                                          Conservative
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             SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.50 inch, 1.4Mb storage
                                                                   Jiangchun
lin, Davin C.
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                                                       COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
                                                                                                                                                                                                                                                                       0.9%;
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Pred. No.
                                                                                                                                                                                                                                                          Mismatches
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701 Fifth Avenue
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                                                                                                                                                                                                                                                         Gaps
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us-09-030-607-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09030607 Patent No. 6262245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                       ZIP: 98104

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CONTINUE OF TOWN NUMBER: US/09/030,607
                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
131,392
                                          REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 AATAAAAATCAACTCAT 500
                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-FEE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                            TELEPHONE:
                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 834 base pairs
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17; Conserv
                                                                                                                                                                                                                                                                                                                         Seattle
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                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, Jiangchun
Dillon, Davin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                              (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David J.
David J.
31,392
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESS
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             682-6031
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                                                              210121.427C3
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SEQUENCE CHARACTERISTICS:

NUMBER OF SEQUENCES:

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RESULT 13
US-08-630-915A-197/c
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GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, NO. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES H
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-439-313-5/c
                                                                                                                                                     Sequence 197, Application US/08630915A Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 834
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Best Local
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APPLICANT:
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APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
CURRENT FILING DATE: 1999-11-12
COURRENT FILING DATE: 1999-11-12
COURRENT FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (1)...(834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                      / Match 0.9%; So Local Similarity 100.0%; For conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AATAAAAATCAACTCAT 30
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanger, Gary
Retter, Mark
Solk, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Day, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang Yuqui
Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harlocker,
FOWLKES, Dana M.

MCCONNELL, Stephen J.

WENTION: POLYPEPTIDES HAVING A FUNCTIONAL

WENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

WENTION: USING SAME
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                      DB 4;
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; Patent NO. ULLOWN GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF NC!
; FILE REFERENCE: RTS-0122
; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
                              γg
                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (133)..(1275)
US-09-444-053-3
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; MOLECULE TYPE:
US-08-630-915A-197
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Best Local S
Matches 17
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                                                               Matches
                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                         LENGTH: 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 971 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
 677
                282 AGGCTCAGGAAGCTTGG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AGGCTCAGGAAGCTTGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 AGGCTCAGGAAGCTTGG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
AGGCTCAGGAAGCTTGG 661
                                                               17;
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                                                             Conservative
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                                                                              0.9%;
100.0%;
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                                                                              Score 17; pred. No.
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                                                               Mismatches
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                                                                              DB 4;
46;
                                                                                                                                                                                                                                                                                                                                      NCK-2 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 971;
                                                                                               Length 1457;
                                                                 Indels
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                                                               Gaps
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US-09-444-053-55

Sequence 55, Application US/09444053A Patent No. 6165728

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US-09-457-708-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
FILE REFERENCE: RTS-0122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/444,053A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 55
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                TELEFAX: (202) 639-661 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Antisense Oligonucleotide
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Scherosis-1 (TSC-1) Gene and Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 AGGCTCAGGAAGCTTG 297
                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                TELEPHONE:
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           STATE:
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6326483
                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                       D.C.
                                                                                                                                                                                                                                                                                                                                                                                                     1455 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van Slegtenhorst, Marjon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sampson, J
Povey, Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kwiatkowski,
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                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                  (202) 639-6585
                                                              639-6604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ski, David J.
Julian R.
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                                                                                                                                                                                                                   US/09/457,708
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Pred. No.
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                                                                                                                                                                                                                                                    Version #1.30
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hes 0;
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; MOLECULE TYPE: I
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-232-144-2
RESULT 18
US-08-230-002-17
; Sequence 17, Application US/08230002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "PCR primer"

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-457-708-21
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US-08-232-144-2/c
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                                                                                                                                                Matches
                                                                                                                                                                 Query Match
Best Local
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Best Local S
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
**PDF 17-74TON NUMBERD: IG/08/932.144
**PDF 17-74TON NUMBERD: IG/08/932.144
                                                                                                                1765 CAGAAATGGAGAATTC 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: ERNST, Barbara G
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1713 ACCTGTCTGAAGGAAG 1728
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                Local Similarity 100.
hes 16; Conservative
                                                                                   27
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nes 16; Conserv
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                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                   CAGAAATGGAGAATTC
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555 13th St, N.W., Suite 701-East
                                                                                                                                                                                                                                                                                                                                             30 base pairs
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100.0%;
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                                                                                                                                                Pred. No. 1. Mismatches
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. 1.3e+02;
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hes 0;
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Best Local Similarity
Matches 16; Conserv
                                                                                              Sequence 17, Appli
Patent No. 5858663
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                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                APPLICANT: NISSON, I APPLICANT: SACCHI, NITITE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPULCE TYPE: CU
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         546 AAATGAAAATCAAGG 561
                                                                                                                                                                                             201 AAATGAAAAATCAAGG 216
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CITY: WASHINGTON
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                             Application US/08678854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 base pairs
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15 L STREET, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
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) 857-0939
NICOLETTA
METHOD FOR THE RAPID AND ULTRA-SENSITIVE
DETECTION OF LEUKEMIC CELLS
: 18
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NICOLETTA
                                                               PAUL E.
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                                                                                                                                                                                                                                                                                                                                                    /note= "Region of homology to human
cyclin D2 region (SEQ ID NO: 18)"
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b; Pred. No. 1.4
0; Mismatches
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hes 0;
                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                   Length 256;
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RESULT 20
US-08-687-080-65/c
; Sequence 65, Application US/08687080
; Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: /note= "Region of homology to human; OTHER INFORMATION: cyclin D2 region (SEQ ID NO: 18)" US-08-678-854-17
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SEQUENCE CHARACTERISTICS:
LENGTH: 256 base pairs
TYPE: nuclei
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                         Best
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                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/230,002
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US/07/954,110
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 12-JUL-19
                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                       APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
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ADDRESSEE: WEIL, GOT
                                                                                                                                                                                                                                                                              546 AAATGAAAAATCAAGG 561
STATE: CA
COUNTRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                               201 AAATGAAAAATCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D
COUNTRY:
                              CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 16; Conserv
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                              ADDRESSEE: Dehlinger & Assucrate 250 STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1615 L S
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOSOME/SEGMENT: T(8;21)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
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103..142
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SYSTEM: PC-DOS/MS-DOS
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2-JUL-1996
201: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                         Human RAD50 Gene and Methods of Use Thereof 175
                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                        0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,680
3ER: 594~112
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                        Score 16; Pred. No.
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                        DB 2; L. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                     Length 256;
                                                                                                                                                                                                                                                                                                                          0;
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
US-08-592-126-137
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 137, Application Patent No. 5821091
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory DITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR EGO ID NO: 65
SEQUENCE CHARACTERISTICS:
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  ZIP: 94306
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 ATGGACTACAAAGTCT 627
                                                                                                                                                                                                                                                                                                        STREET: 350 Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 359 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ATGGACTACAAAGTCT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                        94306
                                                                                                                                                                                                                                                                                           CA
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                                                                                                                                                                                                                                                                                                                          350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                             Dehlinger & Associates
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                                                                                                                                                              Version
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1.4e+02;
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Query Match Best Local : Matches 1

Similarity

0.8%; Score 16; 100.0%; Pred. No.

Conservative

0;

Mismatches

.4e+02;

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0;

Length 595

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; ANTI-SENSE:
US-08-784-289-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
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Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pedrazzini, Thier APPLICANT: Brunner, Hans R TITLE OF INVENTION: Transgen TITLE OF INVENTION: Receptor NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                 TELEFAX: (202) 639-660 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A
REGISTRATION NUMBER: 36,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1361 TTTAGTGATGGGAGTG 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 574 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 639-6585
                                              MOLECULE TYPE:
                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: lin
                                HYPOTHETICAL:
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CITY: Washington
                                                                                                                                                                                                                                                                                    FILING DATE: CLASSIFICATION:
                                                                 TOPOLOGY:
                                                                               STRANDEDNESS: double
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S. ZIP: 20004-1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                LENGTH:
                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08784289
                                                                                                                595 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1455 Pennsylvania Avenue, N.W.
                 NO
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                                                                 linear
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                                              CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic Animals with Disrupted NPY Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 16;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                   US/08/784,289
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1.4e+02;
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US-08-858-207A-116/c
                                                                                Sequence 31, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 643 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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                                                                    APPLICANT:
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                             APPLICANT:
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              PPLICANT:
                                                                                                                                                                                                           696 AAGAAACAGGCTATAA 711
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                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 610-2.
                                                                                                                                                                                 TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
 OF INVENTION:
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: No. 6348328el Compounds F SEQUENCES: 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stodola, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                        Hodgson, John
Knowles, David
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodgson, John
Knowles, David
                                                                     Black, Michael
                                                                                                                                                                                                                                       Conservative
              Stodola, Robert
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                                                                                                                                                                                                                                                                                                                        linear
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09-MAY-1997
                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                 100.0%;
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for Windows Version
No. 6348328el Compounds
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                                                                                                                                                                                                                                                                                                                                                                                             116:
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                    Score 16;
Pred. No
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                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                DB 4;
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                            Sequence 125, Patent No. 634
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017
FILING DATE: 14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                       NUMBER OF SEQUENCES: 534 CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   694 GAACGCCGCGTCAATG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 709 Swederand CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                           COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 GAACGCCGCGTCAATG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
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                                                                                                                                                                          Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             766 base pairs
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                                                                                                                                                                                                                                                     Knowles, David
Lonetto, Michael
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5. 1.4e+02;
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IBM Compatible

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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
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FILING DATE: 24 SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                               REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                    FILING DAIL:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Sholtz, Charles K.
NAME: Sholtz, Charles K.
15.
                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gregory Dolganov TITLE OF INVENTION: TranscriTITLE OF INVENTION: Polypept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250
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              ENGTH:
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: 890 base pairs nucleic acid
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                                                                                              US-08-368-236-2
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Best Local Similarity
Matches 16; Conserv
                                                       Query Match
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                                                                                                                                                                                          TELEFAX: (703) 836-0106 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM
OPERATING SYSTEM: DOS 5.1
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: STELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Richard Steinberg.
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PRIOR APPLICATION NIMBER: 07/941,139
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                            ANTI-SENSE:
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  103 CGTTTCTATCGAAGAC 118
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                                      Local
                                                                                                                          TOPOLOGY:
                                                                                                                                      STRANDEDNESS:
                                                                                                                                                 TYPE: Nucleic Acid
                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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CITY: Alexandria
STATE: VA
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                             Conservative
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Pred. No.
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RESULT 29
US-08-481-130-6/c
; Sequence 6, Application US/08481130
; Patent No. 5702917
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US-08-245-295-6/c
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Best Local Similarity
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/827,689
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NAME: Borun, Michael F.
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APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                               723
                                                                                                                                                                                                                                                                                                                 191 AATTCCCTCCAAGGTG 206
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                               AATTCCCTCCAAGGTG 708
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05-JUN-1992
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100.0%; Pr
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Pred. No.
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RESULT 30
US-08-656-984A-6/c
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; MOLECULE TYPE:
US-08-481-130-6
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Best Local Similarity
Watches 16; Conserv:
                                           Sequence 6, Application US/08656984A Patent No. 5753502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
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PRIOR APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
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PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
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APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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Kilgannon, Patrick D
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05-JUN-1992
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26-MAY-1992
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Pred. No.
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Sequence 6, Application US/08485604
Patent No. 5773293
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WP, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Mater
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Best Local (
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APPLICATION NUMBER: US 0:
FILING DATE: 27-JAN-1992
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MOLECULE TYPE:
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LENGTH: 1295 base pairs
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REFERENCE/DOCKET NUMBER: 270
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                  191 AATTCCCTCCAAGGTG 206
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FILING DATE: 05-AUG-1993
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3: Marshall, O'Toole, Gerstein, Murray & Borun
23 South Wacker Drive, 6300 Sears Tower
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100.0%; Pr
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   Materials
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Pred. No.
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   and Methods
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US-08-487-595-6/c
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                                                                                               Sequence 6, Application US/08487595
Patent No. 5852170
GENERAL INFORMATION:
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Best Local
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall C'Toole, 6300 Sears Tower
                                            APPLICANT: Gallatin, W. Michael APPLICANT: Kilgannon, Patrick D. TITLE OF INVENTION: ICAM-4 Materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1295 base pair
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APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
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                 CORRESPONDENCE ADDRESS:
                                   NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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TELEFAX: 25-3856
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CITY: Chicago
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Marshall,
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22-JAN-1993
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05-JUN-1992
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ER: 27
O'Toole, Gerstein, Murray & Borun
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                                                                                                                                                                                                                                                                                                        Score 16; DB 1; Pred. No. 1.5e+
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                                                   and Methods
                                                                                                                                                                                                                                                                                        1.5e+02;
thes 0;
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US-08-863-790-25/c
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                                                                                                                                               Sequence 25, Application US/08863790 Patent No. 6087130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: US 08/102,852
PRIOR APPLICATION UNMBER: US 08/245 ?~FILING DATE:
FILING DATE: US 08/245 ?~FILING DATE:
                                                                                APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Protein
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1295 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                191 AATTCCCTCCAAGGTG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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               6300 Sears Tower, 233 S. Wacker Drive
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ilarity 100.0%;
Conservative (
                                               Marshall, O'Toole, Gerstein, Murray &
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05-JUN-1992
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; MOLECULE TYPE: US-08-863-790-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/894,061
FILLING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILLING DATE: 22-JAN-193
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6087130and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
ORDEROR APPLICATION DATA:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         APPLICANT: Gallatin, W. Mi
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1295 base pair
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PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                   STREET: 6300 S
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    COUNTRY: U
ZIP: 60606
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                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                   Illinois
                                                                                                                                                       6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1295 base pairs
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

FILING DATE:

APPLICATION NUMBER: US 07/827,689 FILING DATE: 27-JAN-1992

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296,749

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US-08-296-749-25
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                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yuan, L
APPLICANT: Kridl,
APPLICANT: Dehesh,
APPLICANT: Knauf,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08440845D Patent No. 5955329
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Best Local Similarity 100.0%;
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FILING DATE: 22-JAN-193
ATTORNEY,AGENT INFORMATION:
NAME: NO. 6153395and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)474-6300
TELEFAX: (312)474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7:0 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Engineering Plant Thioesterases For TITLE OF INVENTION: Altered Substrate Specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                 APPLICATION NUMBER: US/08/440,845D FILING DATE: 15-MAY-1995
                                                                                                                                                                                           COUNTRY: USA
ZIP: 95616
                                                                                                                                                                                                                                                STREET: 1920
CITY: Davis
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                   CLASSIFICATION:
                                                                                                                                                                                                                                                                      ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
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Kridl, J.
Dehesh, K.
Knauf, V.
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26-MAY-1992
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; Pred. No.
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Best Local Similarity
Watches 16; Conserve
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US-08-868-458-9
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JS-08-868-458-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08868458
Patent No. 6150512
GENERAL INFORMATION:
APPLICANT: Yuan, L.
APPLICANT: Yuan, L.
TITLE OF INVENTION: Engineering plant Thioesterases And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                          INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1058 AGTGATGGGAGTGAAA 1073
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                                                                                                                                                                         APPLICATION NUMBER: 08/537,083
FILING DATE: 29-SEPT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: Microsoft Word For Window
CURRENT APPLICATION DATA:
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/868,458
ETILING DATE: 03-Jun-1997
CLASSIFETCATION: <Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene,
                                 TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                  SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US96/07064 FILING DATE: 15-MAY-96
                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 95616
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                                                                                                                                                          ELEFAX: (916)
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Pred. No.
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US-09-195-940-24
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                                                Sequence 24, Application US/09195940
Patent No. 6258935
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
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Best Local Similarity
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APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
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LENGTH: 1353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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Pred. No
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1.5e+02;
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CITY: BOSTON
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Patent No. 5872094 GENERAL INFORMATION:
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Best Local Similarity
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,078A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MYETS, PAUL L.
REGISTRATION NUMBER: MGP-008
TELECOMMUNICATION INFORMATION:
TET FEBRENCE/DOCKET NUMBER: MGP-008
TELECOMMUNICATION INFORMATION:
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APPLICANT: Tondravi,
APPLICANT: Binette,
TITLE OF INVENTION: M
TITLE OF INVENTION: F
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                               60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tondravi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goetinck, Paul F.
(617) 227-7400
(617) 227-5941
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METHODS FOR PROMOTING CARTILAGE MATRIX
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Pred. No. 1.5e+02;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/0
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MYGTS, Paul L.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-JUNE PRIOR APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
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                          663 ATTACCTCAAGGAAGT 678
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494 ATTACCTCAAGGAAGT 509
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                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                   Local
                                                                                                                                        TOPOLOGY:
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STRANDEDNESS: single
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                                                      Conservative
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                                                                  Score 16;
Pred. No.
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Pred. No.
                                                      Mismatches
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                                                DB 2; 2; 3. 1.5e+02; 0;
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PCT-US94-00253-2
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Best Local Similarity 100.
Best Local Similarity 100.
Conservative
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FILING DATE: 06-JAN-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING:DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PC
                                  FILING DATE: 05-JUN-1992 PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 ATTACCTCAAGGAAGT 678
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STATE: Illinois
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APPLICATION NUMBER: US 0: FILING DATE: 22-JAN-1993
                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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3 South Wacker Drive, Suite 6300
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                    us 08/009,266
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Pred. No.
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J. 1.5e+02;
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Best Local S
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                                                                                                     APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
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SEQUENCE CHARACTERISTICS:
LENGTH: 1472 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,724

APPLICATION NUMBER: US 07/889,724
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
ODERATING SYSTEM: PC-DOS/MG-DOS
ODERATING SYSTEM: PC-DOS/MG-DOS
                                                   FILING DATE: 22-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
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233 South Wacker Drive, 6300 Sears Tower
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                                                     UMBER: US 08/102,852
05-AUG-1993
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MBER: US 08/245,295
18-MAY-1994
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Pred. No.
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US-08-656-984A-9/c; Sequence 9, Appl; Patent No. 57535
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Best Local Similarity
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TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                  APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                              FILING DATE: 18-MAY-PRIOR APPLICATION DATA:
                                                               FILING DATE: 05-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                      FILING DATE: 26-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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LENGTH: 1472 base pairs
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TOPOLOGY: lir
APPLICATION NUMBER: US 08/485,604 FILING DATE: 07-JUN-1995
                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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233 South Wacker Drive, 6300 Sears Tower
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                                                                                                                                                                                                                                                          NUMBER: US 07/889,724
26-MAY-1992
                                                                                                   05-AUG-1993
                                                  18-MAY-1994
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                                                                                                                    US 08/102,852
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Pred. No.
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. 1.5e+02;
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JR. JOSEPH A.

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US-08-485-604-9/c
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Best Local Similarity
Watches 16; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WP, W. Mic
APPLICANT: Kilgannon,
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                    PRIOR APPLICATION NUMBER: US 08/102,852

APPLICATION NUMBER: FILING PARTS
                                                                                                                                                                                                  FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION MINISTER
                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 07/827,689
FILLING DATE: 27-JAN-1992
PRIOR APPLICATION DATA: APPLICATION UMBER: US 07/889,724
                                                                                                                            FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                    APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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TELEFAX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 South Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WENTION: ICAM-4 Materials and Methods
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 NUMBER:
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                       JR. JOSEPH A.
                                                                                                                                                        us 08/009,266
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acker Drive,
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27866/32715
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Pred. No.
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e, 6300 Sears
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US-08-487-595-9/c
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Patent No. 5852170
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Best Local (
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                                                                                                                                                                                                                                                                                        EILING DAIL. 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/827,689
APPLICATION NUMBER: 27-JAN-1992
APPLICATION TATA:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                           APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
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LENGTH: 1472 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gallatin, I
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                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                        APPLICATION NUMBER: FILING DATE: 05-AUG
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                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                   FILING DATE:
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16; Conserv
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3 South Wacker Drive,
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100.0%; Pred. No.
                                                                                                                                                                                       us 08/009,266
                                                                                                                                        US 08/102,852
                                                                                                                                                                                                                                                                                   US 07/889,724
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cker Drive, 6300 Sears Tower
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                27866/32714
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1.5e+(
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s 0;
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INFORMATION FOR SEQ ID NO:

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RESULT 47
US-08-443-568B-15/c
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US-08-443-568B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08443568B Patent No. 5759807
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                                                                                                                                    TELEPHONE: 650-493-493
TELEPAX: 650-493-556
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/443,56
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Abzams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Process for Producing Relaxin NUMBER OF SEQUENCES: 47
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CITY: N
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TYPE: nucleic acid
STRANDEDNESS: single
           NAME/KEY: CDS
LOCATION: 438..1235
                                                                       TOPOLOGY:
                                                                                        STRANDEDNESS:
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                                                                                                                       LENGTH:
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Similarity 100.0%;
16; Conservative (
                                                                                      i: 1500 base pairs nucleic acid DEDNESS: unknown
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1155 Avenue of the Americas
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Daniel, Yansura
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RESULT 49
US-07-759-568-4
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; LOCATION: 438
PCT-US94-06997-15
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; Sequence 15, Application PC/TUS9406997
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                                                          Sequence 4, Application US/07759568 Patent No. 5374506
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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                                            GENERAL INFORMATION:
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APPLICANT: Murphy, TITLE OF INVENTION:
                                                                                                                                                       1474 GCTAGGAGCACGCCAT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: 20-JUN-199
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1474 GCTAGGAGCACGCCAT 1459
                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: United States of America TITLE OF INVENTION: Process for Producing Relaxin NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        874 GCTAGGAGCACGCCAT 889
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 A
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Halluin, Albert REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10036
                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
)EDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 Point San Bruno Boulevard South San Francisco, California
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1994
Philip M.

Cloning of cDNA Encoding a Functional Human Interleukin-8 Receptor
                                                                                                                                                                                                                                    0.8%;
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100.0%; Pred. No.
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Pred. No.
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1.5e+02;
hes 0;
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                                                                                                                                                                                                                                                 Length 1500;
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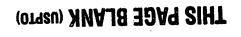
NUMBER OF SEQUENCES:

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RESULT 50
US-08-288-899-1/c
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                                                                                                                                                                                                                                                                                                                                                                                      atent No. 561000:
GENERAL INFORMATION:
GENERAL INFORMATION:
MIURA, MASAMI
CHITAKA
CHITAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 4:
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FILING DATE: 19919913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION UNMBER: 26581
REFERENCE/DOCKET NUMBER: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                   COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn Macpeak and
STREET: 2100 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                     APPLICANT: KAWABE, HARUHIDE
TITLE OF INVENTION: MUTANT A0X2 PROMOTER, MICROORGANISM
TITLE OF INVENTION: CARRYING SAME, METHOD OF PREPARATION THEREOF, AND
TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEIN USING SUCH
TITLE OF INVENTION: MICROORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1510 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CITY: Washington
STATE: D.C.
                                                                                                                                                            CITY: Washington STATE: D.C.
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 APPLICATION NUMBER:
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1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                       ISHIDA, YUTAKA
OI, HIDEYUKI
MURAKAMI, YUKIMITSU
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100.08; F1
US/08/288,899
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                                   Version #1.25
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hes 0;
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US-08-288-899-1
                                                                                                                        TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1528 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                 FEATURE:
                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: plasmid DNA
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                               NAME/KEY:
                                                                                                   TOPOLOGY:
                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                    NAME: Biggart, Waddell A. REGISTRATION NUMBER: 24,861
              LOCATION:
               promoter
1
                                                                                                   linear
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Search completed: June 13, 2002, 12:36:10 Job time: 10738 sec



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Minimum DB
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Perfect score:
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June 13, 2002, 11:00:47; Search time 3439.62 Seconds (without alignments) 12573.529 Million cell updates/sec
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1999
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cgn2_6/pt
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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US-09-633-336-1323
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US-09-633-336-1324
Sequence 20206, A
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US-09-536-784-1
Sequence 1, Application US/09536784
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pn.
NUMBER OF SEQUENCES: 452
NUMBER OF SEQUENCES: Genome Science
    Qy
                                                                      SEQUENCE DESCRIPTION: SEQ US-09-536-784-1
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Matches 1999; Conserv
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                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION OATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
    1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 60
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ADDRESSEE: Human Genome Scients STREET: 9410 Key West Avenue CITY: Rockville
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TYPE: nucleic acid
STRANDEDNESS: double
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                     100.0%; ilarity 100.0%; Conservative
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US-60-353-987-786673
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US-09-526-597A-21
US-09-574-735C-24
US-09-574-735C-29
US-09-765-271-228
US-09-765-271-228
US-09-765-273-228
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US-09-385-222-7
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STREET: 9410 Key West Av		
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RESULT 2 US-09-765-271-1 ; Sequence 1, Application US/09765271 ; GREERAL INFORMATION:	2y 961 ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT 1020	Db Qy
	901 TGTTTCCTT	Db Qy
1921 T 1981 T	841 TGTTGATGT           1   1   1   1   1   1   1   1	Dp QA
1861 A 1921 T	2y 781 TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 840	ОУ ОБ
1801 T	DY 721 AACTGGGATGTGTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT 780	ДУ
	2y 661 TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAACAGGCTATAACCTACTCAC 720 	ОУ
1681	DY 601 ACCAATTACTGATGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 660	p 9
1621	541 A1    541 A1	Db dq
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1501	2Y 421 AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	Qy Db
1441	2y 361 GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 420 	о Оу
1381	DY 301 AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAATAA	Фр
QY 1341 INGGRETACTATARACCARTETATACATARAC	241 TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT 300	Оу
1261 C	29 181 TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC 240	Qy Db
1201	2Y 121 TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180	QУ
1141	2y 61 TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120 	do Qy
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Genome Sciences, West Avenue

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FILING DATE: «Unknown»
APPLICATION NUMBER: 08/961,083
FILING DATE: CCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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MEDIUM TYPE: Diskette, 3.50 incl
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pa
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STATE: Maryland
COUNTRY: USA
ZIP: 20850
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APPLICATION NUMBER: US/09/765,271
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
R APPLICATION DATA:
R APPLICATION DATA:
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Query Match Best Local Similarity

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Score 1999; Pred. No. 0;

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RESULT 3
US-09-765-272-1
; Sequence 1, Application US/09765272
; Sequence 1, Explication US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; TOPPRSPONDENCE ADDRESS:
; SEQUENCE DESCRIPTION: US-09-765-272-1
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                                                                              TELEPHONE: (301) 309
TELEFAX: (301) 309-8:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                               CLASSIFICATION.

PRIOR APPLICATION UMBER: 08/961,083
APPLICATION NUMBER: 08/961,083
EILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: BIOOKES, A. AnderS
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6. SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                        TYPE: nucleic acid
                                        STRANDEDNESS: double
                                                                   LENGTH: 1999 base pairs
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; Sequence 81, Application US/60029960

; GENERAL INFORMATION:
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 10383 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BIOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, i
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/E
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ADDRESSEE: Human Genon
STREET: 9410 Key West
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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Local Similarity
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US-08-961-527-145/c; Sequence 145, Application US/08961527; GENERAL INFORMATION: APPLICANT: Charles Kunsch
TOPOLOGY: US-08-961-527-145
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                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 10711 base pairs
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP VECTRA 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                 NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REEERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                    STREET: 9410 Key West
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                         STRANDEDNESS: double
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                        TACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAATCAGAA
                                       GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT
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RESULT 6
US-09-583-110-1312
; Sequence 1312, Application
; GENERAL INFORMATION:

US/09583110

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FILE REFERENCE: PATHON-OTA
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 1312
LENGTH: 2160
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-583-110-1312
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OF INVENTION: Nucleic Acid and Amino Acid
OF INVENTION: Pneumoniae for Diagnostics
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                       taattacctcaaggaagtcatcaatcaagttgaagaagaaacaggctataacctactcac
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RESULT 8
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; Sequence 9325, Application PC/TUSO203987
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/USO2/03987
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PRIOR APPLICATION NUMBER: 60/26
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 9325
LENGTH: 2160
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TYPE: DNA
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FILE DEFENDED: ELITRA 011A
FILE REFERENCE: ELITRA 011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4
SEQ ID NO 9325
LENGTH: 2160
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US-09-815-242-9325
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US-09-815-242-9325
Sequence 9325, Application US/09815242
GENERAL INFORMATION:
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APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind, Ji
APPLICANT: Wall, Dania
APPLICANT: Trawick, Ji
APPLICANT: Carr, Gran
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1988; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identify
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,85
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                         Sequence 9325, Appliageneral INFORMATION:
                                                                                                APPLICANT:
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Foulkes, J. Gordon
Zamudio, Carlos
Haselbeck, Robert
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Trawick, John D.
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TYPE: DNA
ORGANISM: Streptococcus p
FEATURE:
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NAME/KEY: CDS
LOCATION: (1)...(2160)
JS-10-072-851-9325
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                       TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
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               ttacaatacagacgaatacgttgcctatccagacgatgaattgcaagtcgcttctaccat
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                     AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGA
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
SECURENCE CHARACTERISTICS:
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1988; Conserv
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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APPLICANT: FINNEY, GREGORY L.

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE

TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF

NUMBER OF SEQUENCES: 797

CORRESPONDENCE ADDRESS:
                                          9598
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STREET: 3174 PORTE:
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
              181
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                                                                                                                                                                                                                                                                                                                     LENGTH: 10333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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              TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC
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                                                                                           TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA
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LAGACE, ROBERT E.
CORLEY, NEIL C.
RUSSO, FRANK D.
HANN, AMY L.
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       APPLICANT: Masure, H. Robert
APPLICANT: Pearce, Barbara J.
APPLICANT: Toumanen, Elaine
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SOFTWARE:
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                                                                                       STREET: 411 Hacken
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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NRE: PatentIn Release #1.0, APPLICATION DATA:
                                                                                                                                                                                                                                                                Application US/08116541
                                                                                                                                411 Hackensack Avenue
                                                                                                                                              Klauber & Jackson
            Version #1.25
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; LOCATION:
US-08-116-541-3
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Best Local Similarity
Matches 946; Consert
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
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CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEFAX: 201 343-1684
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CLONE: SPRU42
FEATURE:
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                    AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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Pred. No. 0;
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PCT-US97-14436-139
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                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/14436
FILING DATE: 15-AUG-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Nicholas, Robert
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUC:
TITLE OF INVENTION: POLYPEPTIDES AND THEIR US:
NUMBER OF SEQUENCES: 713
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
EILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 950533
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline B
STREET: 709 Swedeland R
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
                                                               INFORMATION FOR SEQ ID NO:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pairs
TYPE: nucleic acid
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  STRANDEDNESS:
TOPOLOGY: lir
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RESULT 14
US-08-911-503-139
Sequence 139, Application US/08911503
GENERAL INFORMATION:
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Best Local S
Matches 811
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                                                                                           ATCAACAAAATCAGAATCCTCAACCAGCACAACCA
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Pred. No. 1.1e-271;
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Lonetto, Hodgson, John Knowles, David Black, Michael

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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pairs
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REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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MEDIUM TYPE: Diskett
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ADDRESSEE: SmithKline
                        1545 TTGAAAACCACATCAAGACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATA 1604
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nes 811; Conserv
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TTGAAAACCACATCAAGACCTCTCAATTTGTAGCACCTGACGAACTATTTGCTGGCTATA
                                                  ATCTTGCTTGGCTCCCTCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAA
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Pred. No. 1.1e-271;
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                                INFORMATION FOR SEQ ID NO:
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pair
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stodola, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1965 ATCAACAAAATCAGAATCCTCAACCAGCACCAACCA 1999
                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lonetto, Michael APPLICANT: Nicholas, Richar APPLICANT: Stodola Bohert
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                                                  TELEX:
                                                                                                          REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/OFFILING DATE: 15-AUG-1997 CLASSIFICATION: 536
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                                                              TELEFAX:
                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19406-0939
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STREET: 709 Swedeland
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2172 base pairs
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RESULT 16
US-60-068-175-596/c
US-60-068-175-596/c
; Sequence 596, Application US/60068175
; GENERAL INFORMATION:
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APPLICANT:
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Pred. No. 1.1e-271;
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REFERENCE/DOCKET NUMBER: PM-0
TELECOMMUNICATION INFORMATION: (650) 855-0555
TELEPHONE: (650) 845-416
INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
LENGTH: 9845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Finney, Gregory L.
APPLICANT: Finney, Gregory L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1175
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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CLONE: SPN2c598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: INCYT
STREET: 3174 POR
CITY: PALO ALTO
STATE: CALIFORNI.
COUNTRY: USA
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GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA
                                             TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180
                                                                                                                                                                                                                                                                                                                  TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120
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Russo, Frank
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Pred. No. 9.3e-142;
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                                                                                                                                                      Best Local Similarity
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               1384 GTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACACCCTATATGATGACCGACAT 1443
                                                                                   1324 AACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAAAGA 1383
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 323 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/60/029,960 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                   AACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAAAAGA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTG 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAAGCAGTCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGACAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTGAAATGAAAAATCAAGGTTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/60029960
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles Kunsch
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                         double
                                                                                                                                                      11.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae Polynucleotides and Sequences 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                          36,373
                                                                                                                                      0,
                                                                                                                                                      Score 223; DB 41; Pred. No. 4.5e-105;
                                                                                                                                                                                                                                                                                                                                                                                                PB340PP
                                                                                                                                    Mismatches
                                                                                                                                    0;
                                                                                                                                                                    Length
                                                                                                                                    Indels
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PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 1313
LENGTH: 204
TYPE: NAM
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; ORGANISM: Enterococcus faecalis US-09-134-000-1534
                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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US-09-583-110-1313/c
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APPLICANT: Lynn Doworth
                                CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 1534
LENGTH: 2370
TYPE: DNA
                                                                                                                                                                                                                Sequence 1534, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al. TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics FILE REFERENCE: PATHOO-07A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1762 CTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCGTTCTACGTGGAACTCACCTGC 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1942 GCAACAATCAAATACAACCCCTGA 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1882 GTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGACTACCAATCCTAACAATAATAC 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1822 TCCACAACCACCCCCATCAACTGAAAGTTCAAGCTCATCATCAGATAGTTCAACTTCACA 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1444 GATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCCTTGGCTCCCTCA 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 TCCACAACCACCCCCATCAACTGAAAGTTCAAGCTCATCAGCATAGTTCAACTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 CTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCGTTCTACGTGGAACTCACCTGC 145
                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                       84
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; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4e-95;
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US-09-070-927-217
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                                                                                                                                                                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                          2589 TCAAATGCCATTTCAAGTAACACAA 2613
                                                                                                                                                                                                   1226 TCAAATGCCATTTCAAGTAACACAA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: HE TO OPERATING SYSTEM: MSDU OPERATING SYSTEM: MSDU OPERATARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          STRANDEDNESS: do TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: h
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                           Steven Barash
TITLE OF INVENTION: Enterococcus
NUMBER OF SEQUENCES: 982
               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                    nucleic acid
DEDNESS: double
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ADDRESSEE: Human Genome Sciences,
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                                                                                                        Application US/09070927A
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Patrick J. Dillo
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                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (301) 309-8512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                      (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette,
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                                                                                                                                                                                                                                          1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                          Score 25; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                             Mismatches
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                                       faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                     DB 14; Length 8395;
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                                                                                                                                                                                                                                                                                                                     RESULT 22
US-09-536-784-227
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                                                                                                                                                                                                                                                                                         Sequence 227, Applicat
GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                TITLE OF
                                                                                                                                                                                                                                                                                 APPLICANT: Choi et.
                                                                                                                                                                                     STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                            20850
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                                                                                                                                                                                                   Rockville
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-070-927A-217
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2589 TCAAATGCCATTTCAAGTAACACAA 2613
                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

CLASSIFICATION DATA:

ORGANICAL STORAGE

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVEY
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
APPLICATION NUMBER: 08/961,083 FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-850
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06
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                                                                                                                                                                                                                                                                                                                                           Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PB369
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                                                                                                                                                           US-09-765-271-227
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 309
TELEFAX: (301) 309-8:
INFORMATION FOR SEQ ID NO: 227
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 227:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY,AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 227:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
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23; Conserv
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc
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TELEFAX: (301) 309-8512
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1.2%;
100.0%;
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Score 23;
Pred. No.
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Pred. No.
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DB 30;
2.7;
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                                       Length 33;
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                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                          Sequence 108, Applica GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
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INFORMATION FOR SEQ ID NO: 227
SEQUENCE CHARACTERISTICS:
                                                                                                               APPLICANT: APPLICANT:
                               TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECAL:
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1466
CORRESPONDENCE ADDRESS:
                                                                                                                                                       APPLICANT:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4M
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/765,272
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: CURROND>
PRIOR APPLICATION DATA:
ORDER OF THE PRIOR APPLICATION DATA:
ORDER OF THE PRIOR OF THE PRIOR APPLICATION DATA:
ORDER OF THE PRIOR OF THE PRIOR APPLICATION DATA:
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                     ADDRESSEE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 227:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 33 base pairs
                                                                                                           Corely, Neil C.
Russo, Frank D.
Hann, Amy L.
                                                                                                                                                                                                              Application US/60045649
3174 PORTER DRIVE
                                                                                                                                                                      Lagace, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 23; DB ilarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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                                                                                           NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
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309-8512
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Best Local S
Matches 22
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                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/046,653
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
           ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        STREET: 31,3
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF NUMBER OF SEQUENCES: 1449

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                               Lagace, Robert E.
Corley, Neil C.
Russo, Frank D.
Hann, Amy L.
Heath, Joe D.
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                                                                                                                                                                                                                                                                     3174 PORTER DRIVE
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(415) 845-4166
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00.0%; Pred. No.
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PM-0003-1 P
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Best Local Similarity
~+~has 22; Conserv?
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PCT-US02-03987-6631
                                                                                                                                                                                                                              US-09-815-242-6631
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Best Local S
Matches 22
                                                                                                                                                                                             Sequence 6631, Application US/09815242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6631
LENGTH: 2337
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                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US02/03987 CURRENT FILING DATE: 2002-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
             TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                 APPLICANT:
                                                                                                                                                               APPLICANT:
                                                                                                                                                                                APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15811 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 845-4166 INFORMATION FOR SEQ ID NO:
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                APPLICANT:
                                                                                                                APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                             1465 aatgccatttcaagtaacacaa 1486
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 22; Conserv
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                                                                              Carr, Grant J.
Yamamoto, Robert T.
                                                                                                               Wall, Daniel
Trawick, John D.
                                                                                                                                             Ohlsen, Kari L.
Zyskind, Judith W.
                                                                Xu, H. Howard
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100.0%; Pred. No.
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100.0%;
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Query Match

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; NAME/KEY: CDS
; LOCATION: (1).
US-10-072-851-6631
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; LOCATION: (1)...(2337)
US-09-815-242-6631
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                                                                                                        SOFTWARE: Fast
SEQ ID NO 6631
LENGTH: 2337
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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Best Local Similarity
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LENGTH: 2337
                                                                                                                                                         APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                      TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                       FEATURE:
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                                                                                                                                            FastSEQ for Windows Version
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Boone, Charles
                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
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Zamudio, Carlos
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Roemer, Terry
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100.0%; F1
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Pred. No.
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US-09-649-163-2312/c
Sequence 2312, Application US/09649163
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine A.
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                                                                                                  RESULT
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 710:
                                                                                                                                               1229 AATGCCATTTCAAGTAACACAA 1250
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2771 AATGCCATTTCAAGTAACACAA 2750
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: ger
IMMEDIATE SOURCE:
CLONE: EFAlc710
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TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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Holtzman, Douglas A. Galvin, Katherine A. Leiby, Kevin R.
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                                                                                                                                                                                                                 Conservative
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Heath, Joe D.
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                                                                                                                                                                                                                                                                                                                                                                  circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                               genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                               1.1%;
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; Pred. No.
                                                                                                                                                                                                                               Score 22;
Pred. No.
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                                                                                                                                                                                                                                 DB 45;
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APPLICANT:

Kingsbury, Gillian Weich, Nadine S. McCarthy, Sean A.

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; NAME/KEY: misc_feature
; LOCATION: (1)...(537)
; OTHER INFORMATION: n = A,T,C
US-09-652-916-1790
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                                                                                                                                                                                                 SOFTWARE: Fas
SEQ ID NO 1790
LENGTH: 537
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Best Local Similarity
Matches 21; Conserv
Query Match 1.1%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 29 Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Shyjan,
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Fas
SEQ ID NO 2312
                                                                                                                                                                                                                                                                 FILE REFERENCE: 1600.1184-001
CURRENT APPLICATION NUMBER: US/09/652,916
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,103
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: HOVEL NUC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1184-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/649,163
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
PRIOR FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1164-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (1)...(537)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
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Busfield, Samantha J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Villeval, Jean-Luc M.G. Goodearl, Andrew D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MacBeth, Kyle J. Fraser, Christopher C.
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Richardson, Jennifer
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Or
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               DB 25;
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29;
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                               Length 537;
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Gaps
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; TYPE: DNA
; ORGANIZM: Streptococcus pneumoniae
US-09-403-609A-25
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                                                                                                                                                                                                                                                                           Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 46268
SOFTWARE: PERL Program
SEQ ID NO 44152
LENGTH: 242
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR
FILE REFERENCE: PD-1003 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/403,609A CURRENT FILING DATE: 2000-03-03 PRIOR APPLICATION NUMBER: PCT/DE98/01134 PRIOR FILING DATE: 1998-04-22 PRIOR APPLICATION NUMBER: DE 197 17 346.2 PRIOR FILING DATE: 1997-04-24 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HAKENBECK, Regine
TITLE OF INVENTION: DNA PROBES, METHOD AND KIT FOR IDENTIFYING
TITLE OF INVENTION: ANTIBIOTIC-RESISTANT STRAINS OF BACTERIA
FILE REFERENCE: 012627-011
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/535,896
CURRENT FILING DATE: 2000-03-24
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                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01334414
                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                  319 AAAAGCAACCAAGCAAGAAA 338
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36 aaaagcaaccaagcaagaaa
                                                                       / Match 1.0%; Score 20;
Local Similarity 100.0%; Pred. No.
nes 20; Conservative 0; Mismatc
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Delegeane, Angelo M.
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100.0%; Pred. No.
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98;
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                                                                                                            Length 242;
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US-09-515-128-12893/c

Sequence 1

Application US/09515128

GENERAL INFORMATION:

APPLICANT: Arterburn, Matthew

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APPLICANT: Verna, Ron
APPLICANT: Yang, Fei
APPLICANT: Yim, Kenneth
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleer
FILE REFERENCE: 728CIP
CURRENT APPLICATION NUMBER: US/09/515,128
CURRENT APPLICATION NUMBER: 09/09/34,341
EARLLER APPLICATION NUMBER: 09/034,341
EARLLER FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12893
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:

, NAME/KEY: misc_feature

; LOCATION: (1)...(332)

; OTHER INFORMATION: n = A,T,C

US-09-515-128-12893
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                                                                                                                                                                                RESULT
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Best Local S
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APPLICANT: Drake, Jim
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                                                                                             APPLICANT:
                                                                                                                                                                                                                                               1867 TAGTTCAACTTCACAGTCTA 1886
                  APPLICANT:
                                 APPLICANT:
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Similarity 100.0%; F
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Engleman, Carrie
Faulkner, Brandy
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Lomelli, Michelle
Nguyen, Phuong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jessen, Aaron
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Giedt, Gretchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asghari,
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           Bills, Pamela K.
Pham, Mino Thu
Altus, Christina M.
Hillman, Jennifer L.
Ingrid Erika Akerblom
                                                                                            Delegeane,
                                                                                                             Stuart, Susan G
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POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
                                                                                             Angelo
                                                                                                                                                                                                                                                                                                            Score 20; 
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         얹
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                         DB 19;
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                                                                                                                                                                                                                                                                                                                         Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 855, Application US/60001754 GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 845-4166 INFORMATION FOR SEQ ID NO: 8
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1. for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
CLONE: 201668
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1. for Windows/MS-DOS 6.
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: PERIPHERAL BLOOD MACROPHAGES
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AATGGAGAATTCGTATTTAA 205
                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/688,870 FILING DATE:
APPLICATION NUMBER:
                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 39132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                 94304
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                                                                                                                                                                 PALO ALTO
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                                                                                                                                                CALIFORNIA
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                                                                                                                                                                                 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                Bills, Pamela K.
Pham, Mino Thu
Altus, Christina M.
Hillman, Jennifer L.
Ingrid Erika Akerblom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                   Stuart, Susan G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 855-0555
                                                                                                                                                                                                  INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerrone
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us/60/001,754
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Pred. No.
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ATTORNEY/AGENT INFORMATION:

FILING DATE:

NAME: LUTHER, BARBAI REGISTRATION NUMBER:

BARBARA J

33954

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US-09-205-070-44712
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                                                                                                                                                                                                                                                                US-09-321-214-31801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-205-070-44712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748
                                                                                                                                                                                                                         Sequence 31801, Application US/09321214 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/205,070
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44712
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.0%; Score 20;
Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 20; Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                          APPLICANT: Hyseq, Inc.
APPLICANT: Drmanac, Radoje
APPLICANT: Crkvenjakov, Rac
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
         APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Kita, David
APPLICANT: Ford, John
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 855-0195
INFORMATION FOR SEQ ID NO: {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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LENGTH: 355 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                    275 aaaagcaaccaagcaagaaa 294
                                                                                                                                                                                                                                                                                                                                                         319 AAAAGCAACCAAGCAAGAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AATGGAGAATTCGTATTTAA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
REFERENCE: 20411-740
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                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                              Snezana
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                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 371;
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RESULT 41
US-09-516-335-31801
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-746CON1
CURRENT APPLICATION NUMBER: US/09/340,623
CURRENT FILING DATE: 1999-06-28
EARLIER APPLICATION NUMBER: US 09/205,070
EARLIER APPLICATION NUMBER: US 09/205,070
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44712
LEBGTH: 371
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31801
LENGTH: 371
                                                                                                                                                                                                                                                                                           Sequence 31801, Application US/09516335 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
Matches 20; Conservative
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CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: US 60/088,041
EARLIER FILING DATE: 1998-06-02
                                                                  APPLICANT: Giedt, G
APPLICANT: Jessen,
                                                                                                                                                                               APPLICANT: Drake, Jim APPLICANT: Drmanac, Radoje
                                                                                                                                                                                                                   APPLICANT: Dickson, Mark
                                                                                                                                                                                                                                                     APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq, Inc
                    APPLICANT:
                                      APPLICANT:
                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         319 AAAAGCAACCAAGCAAGAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                    275 aaaagcaaccaagcaagaaa 294
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Kita, David
Labat, Ivan
                                    Jomek, Leni
Jones, Lee
                                                                                         Giedt, Gretchen
                                                                                                          Garcia, Veronica
                                                                                                                             Fox, Melvin
                                                                                                                                            Engleman, Carrie
Faulkner, Brandy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                        Aaron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 20;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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98;
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Lomelli, Michelle

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APPLICANT: Wu, James

APPLICANT: Yim, Kenneth

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 740CIP

CURRENT APPLICATION NUMBER: US/09/516,335

CURRENT FILING DATE: 2000-03-01

EARLIER APPLICATION NUMBER: 09/321,214

EARLIER APPLICATION NUMBER: 09/321,214

EARLIER FILING DATE: 1999-05-26

EARLIER FILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 31906

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 31801
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Best Local Similarity 100.0%; Pred. No.
Matches 20; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sidhu, Navjiwan
APPLICANT: Smith, Benjamin
APPLICANT: Smythe, Ashleigh
APPLICANT: Tkach, Joe
APPLICANT: Tran, Lien
APPLICANT: Verna, Ron
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31801, App
GENERAL INFORMATION
                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Nogra, Margie
APPLICANT: Palencia, Servando
APPLICANT: Raisi, Fariba
 APPLICANT
                                                                                                                                  APPLICANT
                                                                                                                                                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Randhwa, Gurpreet
APPLICANT: Sidhu, Navjiwan
APPLICANT: Smith, Benjamin
                  APPLICANT
                                   APPLICANT
                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wachter, Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 AAAAGCAACCAAGCAAGAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 aaaagcaaccaagcaagaaa 294
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                                                                                                                                                                                                                                                                                                                        Asghari, Vida
Damavandi, Simin
Dickson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nguyen,
                                                                               Laroya, Mimi
Lomelli, Michelle
Nelken, Sarah
                           Nguyen, Lynne
Nguyen, Phuong
                                                                                                                                               Jones, Lee
Kita, David
                                                                                                                                                                                                               Giedt, Gretchen
                                                                                                                                                                                                                                               Fox,
                                                                                                                                                                                                                                                                          Drmanac, Radoje
Engleman, Carrie
                                                                                                                                                                                                                                                                                                              Drake, Jim
Palencia, Servando
                                                              Nguyen, Kody
                                                                                                                                                                             Jomek,
                                                                                                                                                                                              Jessen,
                                                                                                                                                                                                                              Garcia,
                                                                                                                                                                                                                                                              Faulkner,
                                                                                                                                                                                                                                                                                                                                                                          Arterburn, Matthew
                Nogra, Margie
                                                                                                                              Labat, Ivan
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                                                                                                                                                                                                                                              Melvin
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                                                                                                                                                                                                                             Veronica
                                                                                                                                                                                              Aaron
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98;
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Query Match
Best Local Similarity
Thes 20; Conserva
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-811-31801
                                                                                                                                               LENGTH: 371
TYPE: DNA
ORGANISM: Homo sapiens
US-09-733-811A-31801
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SOFTWARE: FAST:
; SEQ ID NO 31801
FENGTH: 371
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CURRENT APPLICATION NUMBER: US/09/733,811
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 60/088,041
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 31906
                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 31801 LENGTH: 371
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Best Local Similarity 100.0%;
Matches 20; Conservative
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 31906
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/733,811A CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-740
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APPLICANT: Drmanac, R
APPLICANT: Crkvenjako
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                319 AAAAGCAACCAAGCAAGAAA 338
275 aaaagcaaccaagcaagaaa 294
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Ford, John
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                                                                                                                                                                                                                                                                                                                                                                                                                           Labat, Ivan
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Sidhu, Navjiwan
Smith, Benjamin
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                                                                 Conservative
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                                                                                 100.0%;
                                                                                 1.0%; Score 20;
100.0%; Pred. No.
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Pred. No.
                                                                 Mismatches
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                                                                                 98;
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98;
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                                                                                            Length 371;
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RESULT 44 US-09-898-888-44712

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Sequence 44712, Application US/0989888A

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                             US-09-975-640-31801 : Sequence 31801, Application US/09975640 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 44712
LENGTH: 371
TYPE: DNA
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LENGTH: 371
TYPE: DNA
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Best Local Similarity
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Best Local :
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                                                APPLICANT:
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                                                                                               APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida APPLICANT: Damavandi, Simin
                                                                                 APPLICANT:
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                                  APPLICANT:
                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                    20;
                                                                Dickson, Mark
Drake, Jim
               Drmanac, Radoje
Engleman, Carrie
Faulkner, Brandy
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100.0%; Pred. No. 98;
ive 0; Mismatches
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Best Local S
Matches 20
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APPLICANT:
APPLICANT:
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APPLICANT:
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             Jessen, Aaro
Jomek, Leni
Jones, Lee
Kita, David
                                                                              Garcia, Veronica
Giedt, Gretchen
                                                                                                               Fox, Melvin
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PRIOR APPLICATION NUMBER: 09/73,811
PRIOR APPLICATION NUMBER: 09/733,811
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1998-06-02
NUMBER: 05 SEQ ID NOS: 31906
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31801
LENGTH: 371
TYPE: DNA
ORCANIEW: "
                                                                                                                                       US-09-975-640A-31801 : Sequence 31801, Application US/09975640A ; GENERAL INFORMATION:
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                                                                                                       APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida
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Smith, Benjamin
Smythe, Ashleigh
Tkach, Joe
Tran, Lien
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Nguyen, Phuong
Nogra, Margie
Palencia, Servando
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Labat, Ivan
Laroya, Mimi
Drmanac, Radoje
Engleman, Carrie
Faulkner, Brandy
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Yim, Kenneth
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Wachter, Adam
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Nguyen, Kody
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Giedt, Gretchen
                                                      Drake, Jim
                                                                    Damavandi, Si
Dickson, Mark
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98;
                                                                                                                                                                                                                                                                                                                   0;
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Aaron

Laroya, Mimi

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Sequence 1395, Application US/09271490

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-767
CURRENT APPLICATION NUMBER: US/09/271,490
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 19424
SOSFWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 13695
LENGTH: 378
                                                                                        ; NAME/KEY: misc_feature
; LOCATION: (1)...(378)
; OTHER INFORMATION: n = A,T,C or
US-09-271-490-13695
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                   Best
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       Matches
                                       Query Match
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/733,811
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/088,041
PRIOR APPLICATION NUMBER: 60/088,041
PRIOR FILING DATE: 1998-06-02
NUMBER OF SED ID NOS: 31906
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APPLICANT:
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                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                              TYPE: DNA
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-767
CURRENT APPLICATION NUMBER: US/09/925,552
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/271,490
PRIOR APPLICATION NUMBER: 09/271,490
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 19424
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13695
                                                                                                                                                     ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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US-10-032-354-13695
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13695, Application US/09925552
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-767
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TYPE: DNA
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RESULT 1
US-08-961-083-1
US-08-961-083-1
; Sequence I, Application US/08961083
; GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-961-083-1
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                                                                                                                                                               APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY JAGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: DB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
APPLICATION COMBER: US/08/961,083
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-027-632-4909
US-60-360-039-42617
US-60-360-039-42617
US-09-715-542-5625
US-10-027-632-289703
US-10-027-632-321910
US-10-027-632-321910
US-10-027-632-321125
US-10-027-632-321125
US-10-027-632-297844
US-10-027-632-287844
US-10-027-632-287844
US-10-027-632-287849
US-10-027-632-385403
US-10-027-632-385403
US-10-027-632-185376
US-10-027-632-185376
US-10-027-632-185376
US-10-027-632-3024183
US-10-027-632-204288
US-10-027-632-204288
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5625, Ap.
5625, Ap.
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311458, A.
261931, A.
109123, A.
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Best Local Similarity
Matches 1999; Conserv
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J	TGGGATAG 108	1021 CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAA	Qy	_
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0	_ ,	61 A	0 5	
	ACTATGAA 960	901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACCAAACC	Qy	
	TCAAGTAA 900          TCAAGTAA 900	841 TGTTGATGTTTCTAAGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA 	Db 49	
		188	Qу	
		21 A	Оу	
	CTACTCAC 720          CTACTCAC 720	661 TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAACAGGCTATAACCTACTCAC	Qy	
	TACATGGA 660          TACATGGA 660	601 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 	Оу	
	GTCAATAC 600         GTCAATAC 600	541 ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC 	. Qy	
	TTGGTCTT 540         TTGGTCTT 540	481 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT	Qy Db	
	CAGGCACC 480           CAGGCACC 480	421 AGACCTCAATAATTTÀAGTTTACCTCAGTTAGCCTTGCTGGCTGGAATGCCTCAGGCACC	Qy	
	TATGGTAA 420         TATGGTAA 420	361 GGTCTACATGTCTAATGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 	Qу	
	ATAAATAA 360          ATAAATAA 360	301 AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAATAA	Qy Db	
	GCTTGGTT 300         GCTTGGTT 300	241 TIACTITICAACTICGACTICCGACCAGACTATTICTCGTAAGGCTCAGGAAGCTTGGT1	Qy	
	AAGTTGAC 240         AAGTTGAC 240	181 TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC	Оy	
	TTGCGCAA 180         TTGCGCAA 180	121 TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA	Qy Db	
	GAAGACCA 120          GAAGACCA 120	61 TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 	Qy Db	
	CGCGTCAA 60	1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA	Qу	
	1999; 0; Gaps	ery Match 100.0%; Score 1999; DB 4; Length st Local Similarity 100.0%; Pred. No. 0; Local Similarity 0, Mismatches 0; Indels	Que Bes Mat	

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RESULT 2
US-08-961-083-227
; Sequence 227, Application US/08961083
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
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ATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGAC

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1920 1920 1860

1980 1980 TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCATC

1860

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1801 1801 1741 1741

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US-09-540-209B-4827/c
, Sequence 4827, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
                                                                                                                                        ; TYPE: DNA; B.fragilis; ORGANISM: B.fragilis
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                                                            Query Match
Best Local S
Matches 21
                                                                                                                                                                                    TITLE OF INVENTION: NÜCLEIC ACID AND AMINO TITLE OF INVENTION: FOR DIAGNOSTICS AND THE REFERENCE: 2709 LOOL-001 CURRENT APPLICATION NUMBER: US/09/540,209B CURRENT FILING DATE: 2000-04-04 NUMBER OF SEQ ID NOS: 10444

SEQ ID NO 4827
LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
729
                              986 TTGGAGTACGGTGTCTACGAT 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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NAME: BYOOKES, A. ANDERS
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/961,083
FILING DATE: 30-OCT-1997
CLASSETICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAATCTACGACAATAAAAATC
TTGGAGTACGGTGTCTACGAT
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 33 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
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STATE: Maryland
                                                             Conservative
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TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG

GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT 1680

GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT

1680

TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAAGGAAATTGAAAACCACACCAC 1560

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1500 1440

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AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGA 1440

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TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA 1380

CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTGCCTTACGCTGCCTTTGCAAATGG

CAAAAAATATGGAGCAAGTAGTGAAAAAGATGGCTGCCTTACGCTGTCTTTGCAAATGG

1320 1320 1260 δÃ

CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCCAAGACTTTCCTAAATGGTCTAGG 1200

CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAGG

GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC 1140

1140

1200

1080

AATCGACTACCCAAGTATTCACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA 1260

AATCGACTACCCAAGTATTCACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA

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US-10-027-632-240647
US-10-027-632-240647, Application US/10027632

; Sequence 240647, Application US/10027632

; GENERAL INFORMATION:
    Applicant: Wang, David G.
    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
    TITLE OF INVENTION: Polymorphisms in the Human Genome
    FILE REFERENCE: 10887.129
    CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
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; LOCATION: (1)...(332)
; OTHER INFORMATION: n = A,T,C
US-09-721-544-12893
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US-09-721-544-12893/c
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 12893
LENGTH: 332
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APPLICANT:
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CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 09/515,128
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 09/034,341
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
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APPLICANT: Yang, Fei
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
FILE REFERENCE: 728CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       20;
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Tran, Lien
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Palencia, Serv
Raisi, Fariba
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Lomelli, Michelle
Nguyen, Phuong
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Jones, Lee
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Faulkner, Brandy
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100.0%; Pr
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; Pred. No.
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; LENGTH: 502
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-240648
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; ORGANISM: Human
US-10-027-632-240647
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 240648
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SEQ ID NO 240647
LENGTH: 502
                                                                                     Matches
                                                                                                       Query Match
Best Local
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Best Local Similarity 100.0%;
Matches 20; Conservative
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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                 699 AAACAGGCTATAACCTACTC 718
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147 aaacaggctataacctactc 166
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                                                                                     20;
                                                                                                         Similarity
                                                                                     Conservative
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100.0%; Pr
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Pred. No. 1.7;
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RESULT 9
US-09-620-393B-634/c
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                                                                                                                                  Query Match
Best Local Similarity
"``+ hes 20; Conserva'
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SEQ ID NO 301
LENGTH: 4508
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Best Local S
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SEQ ID NO 214358
LENGTH: 585
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APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: Nucleic acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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                                                                            560 aaaagcaaccaagcaagaaa 579
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RESULT 11
US-10-027-632-98352
; Sequence 98352, Application US/10027632
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US-09-620-393B-8776/c
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                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1068P CURRENT APPLICATION NUMBER: US/09/620,393B CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 9948 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 8776 LENGTH: 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8776, Application US/09620393B GENERAL INFORMATION: APPLICANT: ALEXANDROV, Nickolai et al.
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1068P
CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: Patentin version 3.0
SEQ ID NO 624
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Best Local Similarity 100
Matches 19; Conservative
                                                                                                                                                Best Local Similarity
Matches 19; Conserv
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TYPE: DNA
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OTHER INFORMATION: any n = a,
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LOCATION: 1..428
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: any n =
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Pred. No.
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                                                                                                                                                                 DB 5;
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; ORGANISM: Human
US-10-027-632-250569
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US-10-027-632-250569/c
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                                                                   SEQ ID NO 250569
LENGTH: 1079
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LENGTH: 507
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
DBIOR APPLICATION NUMBER: US 60/167,363
DBIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: 05 60/198,676
PRIOR APPLICATION NUMBER: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                       SOFTWARE: FastSEQ
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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                                                 TYPE: DNA
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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100.0%; Pred. No.
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Query Match

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Score 19;

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Length 1079;

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US-10-027-632-250571/c
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Best Local Similarity
Matches 19; Conserv
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                     APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
                                                            APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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Pred. No.
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US-60-360-039-24027
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; ORGANISM: Xenorhabdus nematophilus
US-60-360-039-23856
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; ORGANISM: Human
US-10-027-632-250571
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Best Local S
Matches 19
                                                                                                                    NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 24027
 Query Match
                                                   TYPE: DNA
ORGANISM: Xenorhabdus
-60-360-039-24027
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SEQ ID NO 23856
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APPLICANT: Chen
APPLICANT: Gold
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Best Local Similarity 100.0%;
Matches 19; Conservative
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                                                                                                                                                  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 388-10(5252)A CURRENT APPLICATION NUMBER: US/60/360,039 CURRENT FILING DATE: 2002-02-21
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                                                                                                      LENGTH: 1299
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Local Similarity 100.0%; Pred. No. 7.1;
hes 19; Conservative 0; Mismatches
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Hinkle, Gregory J.
Slater, Steven C.
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Pred. No.
 Score 19;
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Length 1299;
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42540
LENGTH: 1920
TYPE: DNA
ORGANTO:
                                                                                                                                        ; LENGTH: 166
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyt
US-09-539-331D-25958
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US-60-360-039-42540
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NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 25958
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GENERAL INFORMATION
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Best Local
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Best Local Similarity
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Matches 19; Conserv
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APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
              1284 AAAAGATGGCTGCTGCTT 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GCAAAGCAATTCCCTCCAA 202
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aaaagatggctgctgctt 58
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                                                            1 Similarity
18; Conserv
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ilarity 100.0%;
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Pred. No.
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Pred. No.
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                                                                                          Length 166;
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RESULT 20
US-09-546-210B-30401
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; OTHER INFORMATION: Incyte ID No: hu00209576
US-09-539-800C-2484
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                                                       Sequence 30401, Application US/09540210B
GENERAL INFORMATION:
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 2484
LENGTH: 229
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APPLICANT: Seilhamer,
APPLICANT: Delegeane,
APPLICANT: Stuart, St
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Best Local S
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                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/539,800C CURRENT FILING DATE: 2000-03-30 PRIOR APPLICATION NUMBER: 08/521,383
       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/111 PRIOR FILING DATE: December 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: November 4, 1994 PRIOR APPLICATION NUMBER: 08/943,978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE FILE REFERENCE: PD-1023 CIP
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                                                                                                                                                                                                                                FILING DATE: February 10, 1999
APPLICATION NUMBER: 60/074,364
FILING DATE: February 12, 1998
APPLICATION NUMBER: 09/452,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/993,774
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/034,975
FILING DATE: December 20, 1996
APPLICATION NUMBER: 09/250,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: October 4, 1996
APPLICATION NUMBER: 08/943,979
FILING DATE: October 4, 1997
APPLICATION NUMBER: 60/027,782
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APPLICATION NUMBER: 60/028,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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l Similarity 100.0%;
18; Conservative 0;
Stuart, Susan G.
Stuve, Laura L.
Mullahy, Sara J.
Naughton, Rebecca E.
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Stuve, Laura L.
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PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1991
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OR APPLICATION NUMBER: 60/025,478
OR APPLICATION NUMBER: 60/025,478
OR APPLICATION NUMBER: 08/903,556
OR FILING DATE: July 31, 1997
OR APPLICATION NUMBER: 60/025,217
OR FILING DATE: August 22, 1996
OR APPLICATION NUMBER: 08/937,142
OR FILING DATE: September 23, 1997
OR APPLICATION NUMBER: 60/026,598
OR FILING DATE: September 24, 1996
OR APPLICATION NUMBER: 08/960,746
OR APPLICATION NUMBER: 08/960,746
OR APPLICATION NUMBER: 08/960,746
OR FILING DATE: September 29, 1997
OR FILING DATE: October 29, 1997
                                             APPLICATION NUMBER: 60/039, FILING DATE: February 13, 1 APPLICATION NUMBER: 09/035.
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APPLICATION NUMBER: 08/30.,
FILING DATE: July 31, 1997
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                                                                                                                                                                              FILING DATE: November 22, 1996
APPLICATION NUMBER: 60/007,495
FILING DATE: November 22, 1995
                                                                                                                                                                                                                                                                                                                      FILING DATE: October 29, 1997
APPLICATION NUMBER: 60/030,144
FILING DATE: October 30, 1996
APPLICATION NUMBER: 08/826,847
FILING DATE: April 10, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/905,881
FILING DATE: August 1, 1997
APPLICATION NUMBER: 60/205,204
FILING DATE: August 1, 1996
APPLICATION NUMBER: 08/903,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: May 22, 1
APPLICATION NUMBER: 60
FILING DATE: May 23, 1
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                                                                                                                                                    FILING DATE: November 22, 1 APPLICATION NUMBER: 09/021,
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FILING DATE: June 25,
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NUMBER:
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: March 25, 1996
NUMBER: 08/826,847
: April 10, 1997
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10, 1996
: 08/903,555
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: 60/005,526
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8/862,178
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; OTHER INFORMATION: Incyte ID No: hu01166483
US-09-539-331D-33884
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00789504
US-09-540-210B-30401
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PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER FILING DATE: June 13, 1997
                                                                                                                                                                                                                                  APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNICLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
CURRENT APPLICATION NUMBER: US/9/539,331D
CURRENT FILING DATE: 2000-03-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 33884
LENGTH: 250
TWINE: NESS
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SEQ ID NO 30401
LENGTH: 250
                                                     Query Match
Best Local
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
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 1627 ATGGACAGGCTATTCTAA 1644
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                                                     Local Similarity
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FILING DATE: May 8, 1998
APPLICATION NUMBER: 60/048,431
FILING DATE: May 29, 1997
APPLICATION NUMBER: 09/107,592
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APPLICATION NUMBER: 09/050,817
FILING DATE: March 30, 1998
APPLICATION NUMBER: 60/043,792
FILING DATE: APRIL 11, 1997
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                                      Conservative
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Pred. No.
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Pred. No.
                                      Mismatches
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01253724
US-09-539-800c-15921
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PRIOR FILING DATE: October 4, 1997
PRIOR APPLICATION NUMBER: 60/027,782
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR TILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR FILING DATE: December 20, 1996
PRIOR FILING DATE: February 10, 1999
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
Sequence 16898, Application US/09539800C GENERAL INFORMATION:

APPLICANT: Selihamer, Jeffrey J. APPLICANT: Delegeane, Angelo M. APPLICANT: Stuart, Susan G. APPLICANT: Stuart, Susan APPLICANT: Stuart L. APPLICANT: Mullahy, Sara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PERL Program
SEQ ID NO 15921
LENGTH: 255
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Best Local Similarity
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PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
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PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/111,
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Naughton, Rebecc
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NUMBER: 09/452,
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100.0%; Pred. No.
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RESULT 24
US-09-540-210B-24058
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Best Local Similarity 100.
Matches 18; Conservative
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GENERAL INFORMAT
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LENGTH: 264
                      CURRENT APPLICATION NUMBER: US/09/540,210B CURRENT FILING DATE: 2002-04-03 PRIOR APPLICATION NUMBER: 08/972,899 PRIOR FILING DATE: November 18, 1997 PRIOR APPLICATION NUMBER: 08/395,244 PRIOR APPLICATION NUMBER: 08/395,244 PRIOR PILING DATE: February 27, 1995 PRIOR FILING DATE: September 27, 1996 PRIOR FILING DATE: September 27, 1996
                                                                                                                                                                                                                                            APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
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PRIOR APPLICATION NUMBER: 60/111,
PRIOR FILING DATE: December 10, 1
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
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TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
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OTHER INFORMATION: Incyte ID No: hu01110969
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OR FILING DATE: August 16, 1995
OR APPLICATION NUMBER: 08/271,217
OR FILING DATE: June 27, 1994
OR APPLICATION NUMBER: 08/334,881
OR FILING DATE: NOVember 4, 1994
OR APPLICATION NUMBER: 08/943,978
OR APPLICATION NUMBER: 08/943,978
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** APPLICATION NUMBER: 60/027,782
**FILING DATE: October 4 1007
**APPLICATION OCTOBER 4 1007
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FILING DATE: September 27, 1996 APPLICATION NUMBER: 60/005,526
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APPLICATION NUMBER: 60/028,732
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100.0%; Pred. No.
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JR APPLICATION NUMBER: 60/v...,

JOR APPLICATION NUMBER: 08/903.

JOR APPLICATION NUMBER: 08/903.556

AIOR FILING DATE: July 31, 1996

RIOR FILING DATE: July 31, 1997

PRIOR APPLICATION NUMBER: 60/025,217

PRIOR APPLICATION NUMBER: 08/937,142

PRIOR APPLICATION NUMBER: 08/937,142

PRIOR APPLICATION NUMBER: 08/937,142

PRIOR APPLICATION NUMBER: 60/026,598

TILING DATE: September 23, 1996

TAN NUMBER: 60/026,598
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R APPLICATION NUMBER: 0, 1990
R FILING DATE: OCLOBER: 08/826,847
OR APPLICATION NUMBER: 08/826,847
OR FILING DATE: April 10, 1997
ON TON NUMBER: 60/015,533
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DR FILING DATE: July 31, 1996
DR APPLICATION NUMBER: 08/905,881
DR FILING DATE: August 1, 1997
DR APPLICATION NUMBER: 60/025,204
DR FILING DATE: August 1, 1996
DR APPLICATION NUMBER: 60/903,471
DR FILING DATE: July 30, 1997
DR APPLICATION NUMBER: 60/025,478
DR FILING DATE: July 31, 1996
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JR APPLICATION NUMBER: 08/862,178
JR FILING DATE: May 22, 1997
JR APPLICATION NUMBER: 60/018,217
JR FILING DATE: May 23, 1996
JR APPLICATION NUMBER: 08/881,589
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/041,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/755,524
FILING DATE: November 22, 1996
APPLICATION NUMBER: 60/007,495
FILING DATE: November 22, 1995
APPLICATION NUMBER: 09/021,031
APPLICATION NUMBER: 09/021,031
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FILING DATE: March 25, 1996
APPLICATION NUMBER: 08/826, 847
FILING DATE: APT11 10, 1997
FILING DATE: APT11 10, 1997
APPLICATION NUMBER: 09/074,999
FILING DATE: May 8, 1998
APPLICATION NUMBER: 60/048,431
FILING DATE: May 29, 1997
                                                                                                        APPLICATION NUMBER: 60 FILING DATE: April 11,
                                                                                                                                                             APPLICATION NUMBER: 09 FILING DATE: March 30,
                                                                                                                                                                                                                     FILING DATE: March 14,
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FILING DATE: April 10
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Number: 60/040,431
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NUMBER: 60/039,
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NUMBER: 09/035,172
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10, 1996
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31, 1997
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14, 1997
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L, 1996
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
US-09-540-210B-24058
                                                                                                                                                                            US-09-539-331D-21402
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-919-002-7641
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PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 69/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
                                                                                                                                       Sequence 21402, Application US/09539331D GENERAL INFORMATION:
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APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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Best Local :
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LENGTH: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                          APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA TITLE OF INVENTION: LIBRARIES FILE REFERENCE: 20411-752CON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                       1585 TGAACTATTTGCTGGCTA 1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 tgaactatttgctggcta 91
                                                                                                                                                                                                                                                                                                                                  18; Conservative 0;
INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
                      Naughton,
                    Mullahy, Sara J.
Naughton, Rebecca E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09919002
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Pred. No.
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Pred. No.
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24;
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US-10-027-632-94603
; Sequence 94603, Application US/10027632
; GENERAL IMFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01325546
US-09-539-331D-34826
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; LOCATION: 276, 281
; OTHER INFORMATION: a,
US-09-539-331D-21402
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SEQ ID NO 34826
LENGTH: 296
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Best Local
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Best Local Similarity
Matches 18; Conserv
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LENGTH: 285
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEDIIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/539,331D CURRENT FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 40961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 40961
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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OTHER INFORMATION: Incyte ID No: hu00318340
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                                                                                                                                                                                                             1284 AAAAGATGGCTGCTT 1301
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18; Conser
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Pred. No.
                                                                                                                                                                                                                                                                                        Score 18;
Pred. No.
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24;
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US-10-027-632-94604
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; ORGANISM: Human
US-10-027-632-94603
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PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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                                                                                       Best
                                                                                                      Query Match
                                                                                                                                                                                                                                SEQ ID NO 94604
LENGTH: 457
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/198,676
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                     193 TTCCCTCCAAGGTGGATC 210
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                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/185,218
l Similarity
18; Conservat
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                                                                 Conservative
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Pred. No
                                                                                Score 18;
Pred. No.
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25;
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25;
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US-10-027-632-305499
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US-10-027-632-305498
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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US-10-027-632-305498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 18; Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatc
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 305499
LENGTH: 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Polymorphisms in the FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
                                                                                              PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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                                                                                                        1999-09-28
NIMBER: US 60/146,002
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NUMBER: US 60/146,002
1999-08-09
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US-10-027-632-286371/c; Sequence 286371, Application US/10027632; GENERAL INFORMATION:
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; ORGANISM: Human
US-10-027-632-305499
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    APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TYPE: DNA
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nes 18; Conserv
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APPLICATION NUMBER: US 60/185,218
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llarity 100.0%;
Conservative
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Pred. No.
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Pred. No. 25;
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US-09-620-393B-6548
; Sequence 6548, Application US/09620393B
; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA F
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
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; LOCATION: 318, 328, 347, 398, 400, 411, 423, 425, 429, 439, 443, 445,
; LOCATION: 458, 460, 478, 481, 498, 500, 502
; OTHER INFORMATION: n = A,T,C or G
US-10-097-105-1069
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; ORGANISM: Human
US-10-027-632-286371
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Best Local
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Best Local :
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CURRENT FILING DATE: 2002-03-13
NUMBER OF SEO ID NOS: 1562
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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TYPE: DNA
ORGANISM: Homo sapiens
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l Similarity 100.0%; 18; Conservative 0;
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18; Conserv
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100.0%; Pred. No.
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Pred. No.
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US-10-027-632-81926/c; Sequence 81926, Application US/10027632; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and
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                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human US-10-027-632-135305
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILLING DATE: 2002-04-30
CURRENT FILLING DATE: 2002-04-30
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SEQ ID NO 135305
LENGTH: 532
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Best Local 9
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-028
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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NAME/KEY: misc_feature
LOCATION: 1.526
OTHER INFORMATION: any n =
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les 18; Conserv
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Local Similarity 100.0%;
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 Identification and Mapping of Single Nucleotide
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Pred. No.
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; ORGANISM: Human US-10-027-632-157285
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US-10-027-632-157285/c
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SEQ ID NO 81926
LENGTH: 581
                                                                                  SOFTWARE: FastSEQ SEQ ID NO 157285
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
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                                         TYPE: DNA
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                                                            LENGTH:
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Pred. No.
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Matches Query Match Best Local S

l Similarity 18; Conserv

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0.9%; Score 18; 100.0%; Pred. No.

966 TCACAGACTATGCTCCTG

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; NAME/KEY: Misc_feature
; LOCATION: 1..1281
; OTHER INFORMATION: Ceres Seq. ID no. 1015072
US-09-935-625-18639
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)...(19)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (305)...(305)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                     FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 18639
LENGTH: 1281
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Best Local Similarity
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA00591
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
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CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                          TYPE: DNA
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TYPE: DNA
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1971 AAAATCAGAATCCTCAAC 1988
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                                                                   Similarity 100.0%;
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Pred. No.
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
SEQ ID NO 47071
LENGTH: 123
TYPE: DNA
TYPE: DNA
                Sequence 47214, Application GENERAL INFORMATION:
APPLICANT: Coo, Yongwei APPLICANT: Chen, Xianfeng APPLICANT: Goldman, Barry
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Best Local Similarity
Watches 18; Conserve
                                                                                                    RESULT 43
US-60-360-039-47214
                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bacillus subtilis US-60-360-039-47071
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US-09-935-625-27058
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 27058
LENGTH: 1281
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
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Best Local Similarity
Matches 18; Conserv
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NAME/KEY: Misc_feature
LOCATION: 1..1281
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Chen, Xianfeng
Goldman, Barry S.
Hinkle, Gregory J.
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APPLICANT:

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US-10-027-632-253001/c
; Sequence 253001, Application US/10027632
; Sequence 253001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
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; ORGANISM: Escherichia coli
US-60-360-039-47214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-919-002-13066
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APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13066
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SEQ ID NO 47214
LENGTH: 1299
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                                                             CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                        PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922 PRIOR FILING DATE: FILING DATE: 1999-07-22 PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341 PRIOR FILING DATE: FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1284 AAAAGATGGCTGCTT 1301
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                                                                                                                                                                                                                                                                                                                                                                                                           525 AAAAGATGGCTGCTT 508
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  NUMBER: US 60/185,218
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27;
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                                                                                                         RESULT 47
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APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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US-10-027-632-253003/c; Sequence 253003, Application US/10027632; GENERAL INFORMATION:
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; ORGANISM: Human
US-10-027-632-253001
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; ORGANISM: Human
US-10-027-632-253002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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Best Local
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                      374 AATGGGAACTATGGAATG 391
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                                                                                                                                  704 AATGGGAACTATGGAATG 687
                                                                                                                                                                                                                Local Similarity es 18; Conserv
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100.0%; Pred. No.
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                                                                                                                                                                                                                                    Score 18; ; Pred. No.
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27;
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. 27;
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; ORGANISM: Human US-10-027-632-253004
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US-10-027-632-253004/c
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US-10-027-632-253003
                                                                                                                                                                                 SEQ ID NO 253004
LENGTH: 1555
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Best Local Similarity
Matches 18; Conserv
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SEQ ID NO 253003
LENGTH: 1555
                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/167, 363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156, 358
PRIOR APPLICATION NUMBER: US 60/156, 358
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PRIOR FILING DATE: 2000-07-12
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 AATGGGAACTATGGAATG 687
         18;
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0.9%; Score 18;
nilarity 100.0%; Pred. No.
Conservative 0; Mismatch
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                                                                                                                                                                                                                                                     E: 1999-08-09
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100.0%; Pred. No.
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                           DB 6;
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. 27;
         0;
                                               Length 1555;
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      Gaps
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RESULT 50
US-10-115-123-53
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SEQ ID NO 24796
LENGTH: 1773
TYPE: DNA
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                                                                                                                                                                                                      SEQ ID NO 53
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 94 Human Secreted Proteins FILE REFERENCE: PZ029G30AP1D2 CURRENT APPLICATION NUMBER: US/10/115,123 CURRENT FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A CURRENT APPLICATION NUMBER: US/60/360,039 CURRENT FILING DATE: 2002-02-21
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/089,507 PRIOR FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US99/13418 PRIOR FILING DATE: 1999-06-15
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NAME/KEY: SITE
LOCATION: (940)
OTHER INFORMATION: n equals a,t,g, or (NAME/KEY: SITE
LOCATION: (1279)
OTHER INFORMATION: n equals a,t,g, or (NAME/KEY: SITE)
                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-06-22
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                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                           FEATURE:
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089,510
FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/090,113
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                    2288
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Goldman, Barry S.
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; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2280)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2285)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: 0.9%; Score 18; DB 6; Length 2288;
GUERY Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 1284 AAAAGATGCTGCTGCTT 1301
Db 1734 aaaagatggctgctgctt 1751

Search completed: June 13, 2002, 13:44:17

Job time: 7794 sec
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GenCore version
Copyright (c) 1993 - 2000
4.5
Compugen Ltd.
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OM protein - protein search, using sw model

Run

on: June 13, 2002, 08:40:34; Search time 21.48 Seconds

(without 2979.306 alignments)
Million cell updates/sec

Title: Perfect score: US-08-961-083-2 3484 1 KIYDNKNQLIADLG

Sequence: KIYDNKNQLIADLGSERRVN.....TQQSNTTPDQQNQNPQPAQP 666

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Minimum DB Maximum DB seq length: length: 0 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pir1:\*
pir2:\*
pir3:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

20 20 20 20 20 20 20 20 20 20 20 20 20 2	Result No.
3475 3471 3466 3466 3246 3246 3243 325 325 325 325 325 325 325 32	Score
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penicillin-binding	peptidoglycan glyc	penicillin-binding	penicillin-binding	penicillin-binding	penicillin-binding	penicillin-binding									

## ALIGNMENTS

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95042
A;Status: preliminary R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001 penicillin-binding protein 1A [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001 C;Accession: G95042 A;Cross-references: GB:AE005672; PIDN:AAK74536.1; PID:g14971838; GSPDB:GN00164; TIGR:A;Experimental source: strain TIGR4 A; Molecule type: DNA A; Residues: 1-719 < KUR> B.A.; Morris pneumoniae.

Query Match
Best Local Similarity
Matches 666; Conserva 100.0%; llarity 100.0%; Conservative 0 0; Score 3484; DB 2; Pred. No. 4.6e-194; ); Mismatches 0; Length 719; Indels 0; Gaps

A; Gene: SP0369 C; Superfamily: penicillin-binding protein

C; Genetics:

SP0369

Qγ 밁 Qy Ъ Qy B Qy Ъ δÃ B Qy 174 354 301294 241 234 181 121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180 114 61 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120 54 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60 VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 233 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 173 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 113 413 0;

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penicillin-binding protein la - Streptococcus pneumoniae (strain 45607) (fragment) C;Species: Streptococcus pneumoniae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000 C;Accession: $28038 R;Martin, C.; Sibold, C.; Hakenbeck, R. Martin, C.; Sibold, C.; Hakenbeck, R. Martin, C.; Sibold, C.; Hakenbeck, R. Partine: Relatedness of penicillin-binding protein la genes from different clones of A;Title: Relatedness of penicillin-binding protein la genes from different clones of A;Reference number: $28031; MUID:93010977 A;Accession: $28038 A;Status: translation not shown A;Accession: $28038 A;Status: translation not shown A;Molecule type: DNA A;Cross-references: EMBL:X67873; NID:g47419; PIDN:CAA48073.1; PID:g47420 C;Superfamily: penicillin-binding protein lB
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                                                                                           TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                         TGMDYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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penicillin-binding protein la - Streptococcus peliciles: Streptococcus pneumoniae

C; Species: Streptococcus pneumoniae

C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1

C; Accession: $28037

R; Martin, C.; Sibold, C.; Hakenbeck, R.

EMBO J. 11, 3831-3836, 1992

A; Title: Relatedness of penicillin-binding prot

A; Reference number: $28031; MUID:93010977

A; Accession: $28037

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-719 < WARP>

A; Residues: 1-719 < WARP>

A; Cross-references: EMBL: X67872; NID:947417; PI

C; Superfamily: penicillin-binding protein lB
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                                                                                                                     TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                          SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                        SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                                                                                                    LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
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Pred. No. 2.6e
4; Mismatches
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.6e-193;
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A;Title: Nucleotide sequences of genes encoding penicillin-bi
A and 1B.
A;Reference number: A42893; MUID:92325042
A;Accession: A42893
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
A;Cross_references: GB:M90527; NID:g153766; PIDN:AAA26956.1;
C;Superfamily: penicillin-binding protein 1B
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   KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                                                              TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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Pred. No. 5.1e
3; Mismatches
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5.1e-193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidoglycan glycosyltransferase (EC 2.4.1.129) [imported] - Streptococcus C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: A97913
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C;Keywords:
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A;Residues: 1-719 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99133.1;
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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Ma
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
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                                             VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
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Pred. No. 5.1e-193;
3; Mismatches 1;
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Strain R
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Matsushima, P.;
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penicillin-binding protein la - Streptococcus pneumoniae (strain 5674 C; Species: Streptococcus pneumoniae C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Ma C; Accession: $28034 C; Accession: $28034 C; Hakenbeck, R. 1945 R. Martin, C.; Sibold, C.; Hakenbeck, R. 1946 R. 1956 R. 1957 Reference number: $28031; MUID: $3010977 A; Reference number: $28031; MUID: $3010977 A; A; Status: translation not shown A; Molecule type: DNA A; Residues: 1-719 cMAR> A; Cross-references: EMBL: $67869; NID: $47411; PIDN: CAA48069.1; PID: $4760; Superfamily: penicillin-binding protein 1B
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                                                       VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYYNWDR
                                                                                        SEMKNQGY I SAEQYEKAVNTP I TDGLQSLKSASNY PAYMDNY LKEVI NQVEEETGY NLLT
                                                                                                                                                                                          VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                                           LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
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AYFGNITLQYALQQSRNVTAVETLNKVGLDRAKTFLNGLGIDYPSMHYANAISSNTTESN
                                            VSFGTNQAVETNRDWGSAMKPITDYAPAIEYGVYDSTATMVNDIPYNYPGTSTPVYNWDR
                                                                                                                                                                              VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
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Pred. No. 2.8e
31; Mismatches
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2.8e-180;
nes 22;
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A; Cross-references: EMBL: X67866; NID: 947407; C; Superfamily: penicillin-binding protein 1B
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penicillin-binding protein la - Streptococcus pneumoniae (strain C:Species: Streptococcus pneumoniae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change C;Accession: S28032 C;Accession: S28032 C;R.Martin, C.; Sibold, C.; Hakenbeck, R. Martin, C.; Sibold, C.; Hakenbeck, R. EMBO J. 11, 3813-3836 1992 A;Title: Relatedness of penicillin-binding protein la genes from A;Beference number: S28031; MUID:93010977 A;Beference number: S28031; MUID:93010977 A;Status: translation not shown A;Molecule type: DNA A;Molecule type: DNA
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Score 3245; D
Pred. No. 3.2e
35; Mismatches
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RESULT 8.

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$28031

Spenicilin-binding protein la - Streptococcus pne peniciliin-binding protein la - Streptococcus pneumoniae

C; Species: Streptococcus pneumoniae

C; Date: 17-Apr-1993 #sequence_revision 17-Apr-199;

C; Accession: $28031

R; Martin, C; Sibold, C; Hakenbeck, R.

EMBO J: 11, 3831-3836, 1992

A; Title: Relatedness of penicillin-binding protein A; Reference number: $28031; MUID:93010977

A; Recession: $28031

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-719 <ARR>
A; Residues: 1-719 <ARR>
A; Cross-references: EMBL: X67868; NID:947405; PID.

C; Superfamily: penicillin-binding protein 1B
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           KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
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  KQYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSKKEFSNVGTRAMKETTAYMMTD
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Pred. No. 4.2e-180;
12; Mismatches 22;
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A; Residues: 1-719 < MAR>
A; Cross-references: EMBL: X67867; NID: 947409;
C; Superfamily: penicillin-binding protein 1B
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91.9%; Pred. No. 5.5e-180;
tive 36; Mismatches 18;
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PID: 947410

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RESULT 10
S2B035
penicillin-binding protein 1A - Streptococcus
penicillin-binding protein 1A - Streptococcus
c; Species: Streptococcus pneumoniae
A; Variety: strain 2039
C; Date: 17-Apr-1993 #sequence_revision 17-Apr
C; Accession: S2B035
R; Martin, C; Sibold, C; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A; Title: Relatedness of penicillin-binding pr
A; Reference number: S2B031; MUID:93010977
A; Accession: S2B035
A, Status: translation not shown
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A;Experimental source: strain 2039
C;Superfamily: penicillin-binding protein 1B
C;Keywords: antibiotic resistance; penicillin
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A; Residues: 1-719 <MAR>
A; Cross-references: EMB
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C;Species: Streptococcus pneumoniae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_cha
C;Accession: S28036
R;Martin, C.; Sibold, C.; Hakenbeck, R.
EMBO J. 11, 3831-3836 [1992
A;Title: Relatedness of penicillin-binding protein la genes
A;Reference number: S28031; MUID:93010977
A;Accession: S28036
A;Status: translation not shown
A;Residues: 1-608 <MARD
A;Cross-references: EMBL:X67871; NID:947415; PIDN:CAA48071.1
C;Superfamily: penicillin-binding protein lB
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penicillin-binding protein 1 - Streptococ C; Species: Streptococcus oralis C;Date: 07-Apr-1994 #sequence_revision 07 C;Accession: B42893 R;Martin, C.; Briese, T.; Hakenbeck, R. J. Bacteriol. 174, 4517-4523, 1992 A;Title: Nucleotide sequences of genes en A and 1B.
A;Reference number: A42893; MUID:92325042 A;Accession: B42893 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-637 <MARD A;Residues: 1-637 <MARD A;Residues: 1-637 <MARD A;Cross-references: GB:M90528; NID:g15376 C;Superfamily: penicillin-binding protein
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Best Local S
Matches 511
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|Species: Streptococcus oralis
|Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
                                                                           540
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Local Similarity 87.5%;
nes 511; Conservative
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              13
                                                                                                                                                                                                    MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNI 583
                                                                                                                                                   NVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWD
                                                                                                                                                                                                                                                                                                                        TTGMDYYTNVDQEAQKHLWDIYNTDEYYAYPDDELQVASTIVDVSNGKVIAQLGARHQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                          KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV 179
                                                  MAVWTGYSNRLTPIVGDGFYVAAKVYRSMMTYLSEDDHPGDWTM
                                                                                                    DMMKTVLAYGTGRGAYLPWLPQAGKTGTSNYTDDE1ENYIKNTGYVAPDEMFVGYTRKYS
                                                                                                                                                                                                                                                                                                          TTGMEVYTNVDSKVQQRLWDIYNTDEYVNYPDDELQVASTIVDVTDGKVIAQLGARHQSS
                                                                                                                                                                                                                                                                                                                                                            {\tt LSEMKGQGYITAEQYEKAINTPITDGLQSLKSANSYPPYMDNYLKEVIDQVEQETGYNLL}
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Pred. No. 1.2e-148;
9; Mismatches 33;
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       penicillin-binding protein 1A [imported] - Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: G8692 C;Accession: G8692 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbac Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: C; Genetics:
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Best Local Similarity 52.1%;
Matches 333; Conservative 10
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                                                                                                                                                                                                                                                                              GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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                 KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKGGSLNGGSTLDMQLIKLSFFSTDESDQTLSVKIQEAWMALKLDQKWTKEQIFTAYVNK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYTPQYSMAVWTGYSNRMTPIYGTSTQIATKVFSSMMTQLTPDPSSVATWTMPEGVSQEG
                                                                               GYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMYTYLS-EGSNPEDWNIPEGLYRNG
                                                                                                                                                 MMKTVLTY----GTGRNAYLAWLPQAGKTGTSNYTDEEI----ENHIKTSQFVAPDELFA 532
                                                                                                                                                                                                                                                                  TYFGSMTVKSALALSRNIPAVKTLINVGLDNSSKFVNGLGITLDPLEYSNAISSNS----
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                                                                                                                                ILQSVLTLPLSESVGSYAAVPGLAAAGKTGTSNYTDSEMDQITEKYGSLPGMVSPDENFV
                                                                                                                                                                                                                                                                                                                                VTFGFNQAVQTDRDWGSTMKPIVDYGPAFENNIYTSTNNYVSDSPTTYP-NGTPLKNWDN
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Pred. No. 2.6e
D5; Mismatches
-TDSSGQTISQSSA
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RESULT 14
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(C): Species: Listeria monocytogenes (str. C): Species: Listeria monocytogenes (str. C): Species: Listeria monocytogenes (Species: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

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R;Glaser, P.; rranyum, Durand, E.; Durand, L.; Pussuryum, D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-827 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99970.1; PID:gl6411345; GS:
A:Fynerimental source: Strain EGD-e
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A; Gene:
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
R: Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
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                                                                                                                                                                                                                                                                    ESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDG-SEKEFSNVGTRAMKETTAY
                                                                                                                                                                                                                                                                                                      FGYKGPISVRQALYQSRNIPALKTLQAVGLDKSEEFVNKLGITYDEGQNVESNAIGANS-
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                                                                                                                    EFVFKNGARSTWNSPAP----QQPPSTESSSSSSSSSTSQ--SSSTTPSTNNSTTTNPNN
                                                                                                                                               AGYTTNYSIAVWTGYDDKKKYVSASEQKIAQRMFSKLMAHASAGKTTADFKMPSNVV---
                                                                                                                                                                                                                           MMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAP-----DELF
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                                                                 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.9%; Score 1217; I
ilarity 40.3%; Pred. No. 1.2e
Conservative 133; Mismatches
                                                                                          SVPILKGSNPIARAAQGTSSDKVSYELFLSGTAPTKTASTPEDEKK
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1.2e-62;
hes 210;
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RESULT

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Science 294, 849-852, 2001
A; Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MÜID:21537279; PMID:11679669
A; Accession: AD1683
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-826 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC97236.1; PID:g16414507; GSPDB:A; Experimental source: strain Clip11262
C; Genetics:
A; Gene: pbpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             penicillin-binding protein 2A homolog pbpA [imported] - Listeria innocua (strai) C;Specles: Listeria innocua (c;Specles: Listeria innocua (c;Specles: Listeria innocua (c;Specles: Listeria innocua (c;Specles: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AD1683
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; J.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 264; Conserv
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VPILKG-----SNPIARAAEGTASDKVSYELFLSGTAPTKTASTPEDEKKKAEEEAKKK
                                                                                                                                                                                                                                                                                             AGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNG
                                                                                                                                                                                                                                                                                                                                                                                                   MVSDVLKDVLSVGTGTTAAVPGVPAAGKTGTTNIPPE----FTSKYYYPSGAARDSWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAP----DELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGYKGPISVRQALYDSRNIPALKTLQAVGLDKSEQFVNKLGITYDKGQNVESNAIGANS-
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                                                                                           EFVFKNGARSTWNSPAPQQPPSTESSSSS-----SDSSTSQSSSTTPSTNNSTTTNPNNN
                                                                                                                                                                                                 AGYTTNYSIAVWTGYDDKKKYVSASEQKIAQRMFSKLMAHVSANKTTTDFKMPSNVV--S
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Voss, H.; Wehla
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Db 709 AEEDKKKTEEEKKKEEEAK 727

Search completed: June 13, 2002, 08:41:08 Job time: 34 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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3484
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                                                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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                                                                                               sp_rodent:*
                                                                                                             sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length I	DB .	ID	Description	iption
ב	3484	100.0		2	Q9REU0	Q9reu0	) streptococc
2	3468	99.5		N	Q9RET9	Q9ret9	
w	3403	97.7		N	Q9RET3	09ret3	
4.	3329	95.6		Ν	OMAM60	Q9wvw0	
ъ	3314	95.1	719	N	Q9RET8	Q9ret8	~
σ	3299	94.7		2	Q9WW11	Q9ww11	
7	3274	94.0		N	Q9RET4	Q9ret4	-
89	3247	93.2		N	Q57114	Q57114	-
9	3246	93.2		Ν	Q9RET6	Q9ret6	
10	3246	93.2		2	Q54949	Q54949	
11	3245	93.1		N	Q54947	Q54947	
12	3243	93.1		N	Q54946	Q54946	
13	3241	93.0		N	Q54948	Q54948	
14	3231	92.7		N	Q9RET5	Q9ret5	streptococc
15	3192	91.6		N	Q54950	054950	_
7	ע ער 4	2				******	

## ALIGNMENTS

ОУ	Qu Be	SQ	뮸	DR	DR	DR	DR	RĽ	RT	RT	RΤ	RA	RX	RC	RΡ	RN	o <b>x</b>	റ്റ	8	SO	GN	DE	DΤ	DT	DT	AC	ij	RESULT
1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60 	Query Match 100.0%; Score 3484; DB 2; Length 719; Best Local Similarity 100.0%; Pred. No. 2.1e-181; Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 719 AA; 79758 MW; 5BD397E83B4B3AA6 CRC64;	Ptam; PF00905; Transpeptidase; 1. ProDom; PD001895; Transqlycosyl; 1.	Pfam; PF00912; Transglycosyl; 1.	InterPro; IPR001460; Transpeptdse.	InterPro; IPR001264; Transqlycosyl.	EMBL; AF210745; AAF17255.1;	J. Med. Microbiol. 50:828-832(2001).	serotype 23F from the nasopharyngeal flora of children.";	occus	"Alterations to penicillin-binding proteins 1A, 2B and 2X amongst	Ferroni A., Berche P.;	MEDLINE=21432820; PubMed=11549185;		SEQUENCE FROM N.A.	[1]	NCBI_TaxID=1313;	Streptococcus.	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	Streptococcus pneumoniae.	PBP1A.	PENICILLIN-BINDING PROTEIN 1A.	(TrEMBLrel. 19,	(TrEMBLrel. 13,	01-MAY-2000 (TremBLrel. 13, Created)	Q9REUO;	Q9REUO PRELIMINARY; PRT; 719 AA.	TO 1
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Ferroni A., Berche P.;

"Alterations to penicillin-binding proteins 1
penicillin-resistant clinical isolates of Str
serotype 23f from the nasopharyngeal flora of
J. Med. Microbiol. 50:828-832(2001).
1 Med. Microbiol. 50:828-832(2001).
2 Pfam; pr00912; Transglycosyl; 1.
3 Pfam; pr00905; Transglycosyl; 1.
3 Probom; PD001895; Transglycosyl; 1.
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01-MAY-2000 (TIEMBLIEL. 13, L
01-DEC-2001 (TIEMBLIEL. 19, L
PENICILLIN-BINDING PROTEIN 1A
                                                                                                              STRAIN-SP 1513;
                                                                                                                      SEQUENCE FROM
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Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                    MEDLINE=21432820; PubMed=11549185;
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NCBI_TaxID=1313;
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PENICILLIN-BINDING PROTEIN 1,
 SEQUENCE FROM N.A. STRAIN=BM 4200; MEDLINE=21432820;
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"Alterations to penicillin-binding proteins 1A, 2B and 2X a penicillin-resistant clinical isolates of Streptococcus pne serotype 23f from the nasopharyngeal flora of children.";

L. J. Med. Microbiol. 50:828-832(2001).

REMBL; AF210752; AAF17262.1; -.

RINTERPRO; IPR001264; Transglycosyl.

RINTERPRO; IPR001264; Transglycosyl.

RINTERPO; IPR001460; Transpeptdse.

Pfam; PF00912; Transglycosyl; 1.

RPfam; PF00905; Transpeptidase; 1.

RPfam; PF00905; Transpeptidase; 1.

RP FroDom; PD001895; Transglycosyl; 1.

SO SEQUENCE 719 AA; 79781 MW; DB5993F6BD47F72D CRC64;
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Similarity 97.3%;
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CONTRILING. AND PO-341;
CONTRILING-342, PO-273, AND PO-341;
CONTRILING-342, PO-273, AND PO-341;
CONTRILING-342, PO-273, AND PO-341;
CONTRILING-342, PO-273, AND PO-341;
CONTRILING AND PO-341;
CONTROL AND PO-341
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Streptococcus pneumonia
Bacteria; Firmicutes; I
Streptococcus.

NCBI_TaxID=1313;
[1]
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Local Similarity 94.4
hes 629; Conservative
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PO-273,
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s; Pred. No. 5.6e
25; Mismatches
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J. Med. Microbiol. 50:828-832(2001).

R EMBL, AF210747; AAF17257.1; -.

R InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transgptdse.

R InterPro; IPR0014760; Transpeptdse.

R Pfam; PF00912; Transglycosyl; 1.

R Pfam; PF00912; Transglycosyl; 1.

R Pfam; PF00915; Transglycosyl; 1.

R ProDom; PD001895; Transglycosyl; 1.

SEQUENCE 719 AA; 79662 MW; A7B96EA15434A805 CRC64;
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O9RET8;
O1-MAY-2000 (TremBlrel. 13, C)
O1-MAY-2000 (TremBlrel. 13, L)
O1-DEC-2001 (TremBlrel. 19, L)
TENTOTILIN-BINDING PROTEIN 12
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EMBL; AF139890; AAD43073.1; -.

EMBL; AF139887; AAD43070.1; -.

EMBL; AF139888; AAD43071.1; -.

EMBL; AF139889; AAD43071.1; -.

EMBL; AF139889; AAD43072.1; -.

EMBL; AF159488; AAD4430.1; -.

InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transpeptdse.

pfam; PF00905; Transpeptdses; 1.

PfoDom; PD001895; Transglycosyl; 1.

SEQUENCE 719 AA; 79701 MW; 3EDC8A:
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01-NOV-1999 (TrEMBL:
01-NOV-1999 (TREMBL:
01-JUN-2001 (TREMBL:
PENICILLIN-BINDING)
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Microbiology 0:0-0(1999).
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type 14 variants of the Spanish penicillin-resistant serotype
of Streptococcus pneumoniae arose by large recombinational
coments of the cpsA-pbpla region.";
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                                        penicillin-resistant clinical isolates of Streptoco
serotype 23F from the nasopharyngeal flora of child
J. Med. Microbiol. 50:888-832(2001).
EMBL; AF210751; AAF17261.1; -
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79567 MW; 7B6EDCCBB8BCF286 CR
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Streptococcus pneumonia
Bacteria; Firmicutes; 1
Streptococcus.
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Q9RE74;
01-MAY-2000 (TrEMBLrel. 13, Create
01-MAY-2000 (TrEMBLrel. 13, Last;
01-DEC-2001 (TrEMBLrel. 19, Last
                                                                                                         Q9RET4
                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=SP 22861;
                                                                                                                                                                                NCBI_TaxID=1313;
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Mismatches
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749095; CAA88918.1; -.
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01-NOV-1996 (TrEMBLrel. 01, I
01-JUN-2001 (TrEMBLrel. 17, I
PENICILLIN-BINDING PROTEIN 1A
                                                                                                                              STRAIN-CS111 (CEPHALOSPORIN-RESISTANT MEDLINE=96012191; PubMed=7574521; Coffey T.J., Daniels M., McDougal L.K.
                                                                                                                                                                                                                                                                                Streptococcus
Bacteria; Fir
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NCBI_TaxID=1313;
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Best Local Similarity 91.9
Matches 612; Conservative
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptdase; 1.
ProDom; PD001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79712 MW; 539660
PBP1A.
Streptococcus pneumoniae.
Racteria; Firmicutes; Bac
                                O9RET6 PRELIMINARY; PRT; 719 AA.
09RET6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PENTCILLIN-BINDING PROTEIN 1A.
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91.9%;
        Bacillus/Clostridium
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33; Mismatches 21;
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       group; Streptococcaceae;
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NCBI_TaxID=1313;
[1]
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Pred. No. 1.8e
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InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PF00905; Transpeptidase; 1.
ProDom; PF001895; Transglycosyl; 1.
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EMBO J. 11:3831-3836(1992).
EMBL; X67869; CAA48069.1; -
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Martin C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein la
clones of penicillin-resistant Streptococcus
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NCBI_TaxID=1313;
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Martin C., Sibold
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AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
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BLrel. 17, Last annotati
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Pred. No. 1.8e-168;
1; Mismatches 22;
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"Relatedness of penicillin-binding process of penicillin-resistant Streptt South Africa and Spain.";

EMBO J. 11:3831-3836(1992).

EMBL; X67866; CAA48066.1; -.

InterPro; IPR001264; Transpeptdse.

Pfam; PF00912; Transglycosyl; 1.

Pfam; PF00902; Transglycosyl; 1.

Pfam; PF00905; Transglycosyl; 1.

ProDom; PD001489; Transglycosyl; 1.

ProDom; PD001895; Transglycosyl; 1.

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SEQUENCE 719 AA; 79710 MW; D90EB42
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NCBI_TaxID=1313;
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  GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                       VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDR
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Coffey T.J., Daniels M., Enright M.C., Spratt B.G.;
"Serotype 14 variants of the Spanish penicillin-resistant clone of Streptococcus pneumoniae arose by large recombina replacements of the cpsA-pbpla region.";
Microbiology 0:0-0(1999).
EMBL; X67868; CAA48068.1; -.
EMBL; AF046230; AAC24695.1; -.
EMBL; AF046230; AAC24695.1; -.
EMBL; AF03983; AAD43066.1; -.
EMBL; AF139883; AAD43066.1; -.
EMBL; AF139883; AAD43066.1; -.
                                                                                                                                                                                                                    "Association of a thr-371 substitution of penicillin-binding protein 1A with p Streptococcus pneumoniae."; Antimicrob. Agents Chemother. 42:2267-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-30(1997); PubMed=1396576;
MEDLINE-30(1997); PubMed=1396576;
Martin C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein la genes from differen clones of penicillin-resistant Streptococcus pneumoniae isolated South Africa and Spain.";
EMBO J. 11:3831-3836(1992).
                                                                                                                                                                                                                                                                                        SEQUENCE OF 320-717 FROM N.A. STRAIN-#17/Z46, #20/B98, AND #27/SHA3; MEDLINE-98409715; PubMed-9736547; Asahi Y., Ubukata K.;
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Pfam; PF00912; Transpeptidase; 1.

Pfam; PF00905; Transpeptidase; 1.

ProDom; PD001895; Transglycosyl; 1.

NON_TER 719 719

SEQUENCE 719 AA; 79736 MW; F090
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Q54948;
Q54948;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last seq)
Q1-JUN-2001 (TrEMBLrel. 17, Last ann)
PENICILLIN-BINDING PROTEIN 1A (FRAGM)
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91.9%;
                 Bacillus/Clostridium
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Pred. No. 2.7e
32; Mismatches
                                                     Last sequence up Last annotation (FRAGMENT).
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clones of penicillin-resistant Streptococcus pneumoniae isc

South Africa and Spain.";
LEMBO J. 11:3831-3836(1992).
EMBD; X67867; CAA48067.1; -.
InterPro; IPRO01264; Transpeptdse.
R InterPro; IPRO01264; Transpeptdse.
R InterPro; IPRO01269; Transglycosyl; 1.
Pfam; PP00912; Transpeptdses; 1.
Pfam; PP00905; Transpeptdses; 1.
Pfam; PP0091895; Transpeptdses; 1.
ProDom; PD001895; Transglycosyl; 1.
R ProDom; PD001895; Transglycosyl; 1.
PSCOUNTER 719 719
SEQUENCE 719 AA; 79611 MW; 1DBFDDA93704930B CRC64;
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                                                     STWNSPAPQQPPSTESSSSSSSSSSSSSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
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                                                                                      AVWTGYSNRLTPIVGDGFLVAAKVYRSMITYLSEDTHPEDWTMPDGLFRNGEFVFKNGAR
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ilarity 91.9%;
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Pred. No. 3.4e-168;
86; Mismatches 18;
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"Alterations to penicillin-binding proteins IA, 2B and 2X in penicillin-resistant clinical isolates of Streptococcus professoritype 23F from the nasopharyngeal flora of children.";

J. Med. Microbiol. 50:828-832(2001).

EMBL; AF210750; AAF17260.1;

InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transgeptdse.

InterPro; IPR001460; Transgeptdse.

Pfam; PF00905; Transgeptdses; 1.

Pfam; PF00905; Transgeptdses; 1.

Pfam; PF000912; Transglycosyl; 1.

SEQUENCE 719 AA; 79734 MW; 3BE77571DBC86496 CRC64;
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Q9RET5;
Q1-MAY-2000
01-MAY-2000
01-DEC-2001
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NCBI_TaxID=1313;
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Streptococcus pneumon
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STRAIN-SP 1470;
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                                                                                     MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM
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Pred. No. 1.2e
34; Mismatches
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.2e-167;
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Martin C., Sibold C., Hakenbeck R;

Martin C., Sibold C., Hakenbeck
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01-NOV-1996 (TremBLrel. 01, Last sequence up
01-JUN-2001 (TremBLrel. 17, Last annotation
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
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Bacteria; Firmicutes; Bac
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                                                                                                                                                                                                                                                    Sequence 6, Application Patent No. 6027906 GENERAL INFORMATION:
ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: Patentin Release #1.0, \

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,435

FILING DATE: 10-JUL-1995

CLASSIFICATION: 435
                                                                                                                                                                                                   APPLICANT: Balganesh, Ta
APPLICANT: Town, Christi
TITLE OF INVENTION: NO.
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                              ADDRESSEE: White
STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: United S
ZIP: 10036-2787
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                                            PatentIn Release #1.0, Version
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REFERENCE/DOCKET NUMBER: 1103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 662
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FILING DAYE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILLING DAYE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
                                                                                                                                                                                                                                                                                                                                        137
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TOPOLOGY: linear
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                                                          SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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   POPAOP
                                 STWNSPAPQQPPSTESSSSSSSSSSSSSTTPSTNNSTTTNPNNNTQQSTTTPDQQNQN
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                                                                                                                                                                                                                                                                                                                                          VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                     STWSSPAPQQPPSTESSSSSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
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   666
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Pred. No. 5
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-245-511-4
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US-08-245-511-4
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Best Local Similarity
Matches 315; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                  185
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CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/O FILING DATE: 18-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/116,541
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                                                                                                          SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
                                                         TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
                                                                                                                                                                                  VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 184
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   VSFGINQAVETNRDWG
                                     TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 1621; DB 2; Length 320; 99.7%; Pred. No. 6.7e-115; tive 0; Mismatches 1; Indels
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
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TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
181 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETTGYNLLT 240
                                                        125
                                                                   121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
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                                                                                                                                            61 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 18-MAY-1994
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FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                   Match 46.5%;
Local Similarity 99.7%;
les 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 411 Hack
CITY: Hackensack
                                                                                                                                                                                              LENGTH:
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                                                                                                                           LQSNSLQGGSALTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 124
                                                      VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 184
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5981229
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                                                                                                                                                                                                                                                                                                                                                                                                                                  320 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klauber & Jackson
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                                                                                                                                                                                                                                                                   Score 1621; DB 2;
Pred. No. 6.7e-115;
0; Mismatches 1;
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RESULT 5
US-08-731-716-2
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Penicillin Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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CITY: In
STATE: I
COUNTRY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                            95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                       2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61 |:| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                               TGMDYYTNYDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                       TAGRSGGGSTITQQLAKNAYLS---QDQTVERKAKEFFLALELSKKYSKEQILTMYLNNA 208
                                                                                                                                                                               TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 304
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EMKNQGYISAEQYEKAVNTPIT----DGLQSLKSASNYPAYMDNYLKEVI----NQVEEET
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Lilly Corporate Center
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No. 5789202ris, Franklin H.
VVENTION: Penicillin Binding Protein From
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Rockey, Pamela K.
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                                                                                                                                                       APPLICATION NUMBER: IN 580/MAS/94
FILLING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                          REFERENCE/DOCKET NUMBER: 1103326-151 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 / CITY: New Yor
                                                                             REGISTRATION NUMBER:
                                                                                                    NAME: Sterner, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGKTGTT----EAVFNPEYTS-----DQWVIGYTPDVVISHWLGFPTTDENHYLAGSTSN
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10036-2787
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Matches 202; Conserv
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INFORMATION FOR SEQ ID NO: :
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LENGTH: 828 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                  NNSTTTNPNNNTQQ---SNTTPDQQ 657
                                                                                                                                                                        VAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIP 584
                                                                                                                                                                                                                      TPLAFLIKSALNTNIFGEPGWQGTGWRAGRDLQRRDIGGKTGTTN~
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                                                                                                          EGLYRNGEFVFKNGARSTWNS------PAPQQP--PSTESSSSSSDSSTSQSSSTTPST 635
                                                                                                                                               SSKDAWFSGYGPGVVTSVWIGFDDHRRNL---GHTTASGAIKDQISGYEGGA-----
                                                                                                                                                                                                                                                                                                                                    ----SEKEFSNV-----GTRAMKETTAYM-MTDMMKTVLTYGTGRNAY-----
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                                                                                                                                                                                                                                                                                                                                                                                                        TESDKKYGASS---EKMAAAYAAFANGGTYYKPMYIHKVVFSDG---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QALRQVGSNIKPFL-YTAAMDKGL--TLASMLND------VPISRWDASAGSDWQPK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYBGTNTPVYNWDRG------
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-LANGGNSREEYFIEGTQPTQQ 809
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US-08-481-435-10
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IN 580/MAS/94 ETLING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2 ETLING DATE: 24-NOV-1994
ATTORNEY_AGENT INFORMATION:
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 354-81: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Esch
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
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NUMBER OF SEQUENCES:
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226
                              180 LSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEE---ETGY 236
                                                              166
                                                                                                                               109
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                            Local Similarity
nes 200; Conserv
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                                                                                                                                              NLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                                              KIYLGYRAYGVGAAAQVYFGKTVDQLTLNEMAVIAGLPKAPSTFNPLYSMDRAVARRNVV
                                                                                                                             LFSGHASQGASTITAALARNFFLS---PERTLMRKIKEVFLAIRIEQLLTKDEILELYLN 165
                                                                                                                                                                                            QIYSADGELIAQYGEKRRIPVTLDQIPPEMVKAFIATEDSRFYEHHGVDPVGIFRAASVA 108
                                                                               KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV 179
LSRMLDEGYITQQQFDQTRTEAINANYHAPEIAFSAPYLSEMVRQEMYNRYGESAYEDGY
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10036-2787
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129; Mismatches 246;
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                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08481435 Patent No. 6027906
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         636
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                                                                                                                                                                       STATE: New York COUNTRY: United States ZIP: 10036-2787
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                              APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995 CLASSIFICATION: 435
                                                                                                                                                                                                      CITY: New York
STATE: New Yor
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NUMBER:
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; MOLECULE TYPE: protein
US-08-481-435-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: SE 9
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
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                           SSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQNPQPAQ
                                                                   LA-NQTPTPLNLVPPEDIADMGVDYDGNFVCSGGMRILPVWTS----
                                                                                                      LSEGSNPEDWNI--PE----GLYRNGEFVFKNGAR--STWNSPAPQQPPSTESSSSSSD
                                                                                                                                      ----NNV----DTWFAGIDGSTVTITWVGRDNN-QPTKLYGASGAMSIYQ---RY
                                                                                                                                                                         DEETENHIKTSOFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTY
                                                                                                                                                                                                             DGKVLYQSFPQ-AERAVPAQAAYLTLWTMQQVVQRGTGRQLGAKYPNLHLAGKTGTTN--
                                                                                                                                                                                                                                                DGS--EKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGR--NAYLAWLPQAGKTGTSNYT 511
                                                                                                                                                                                                                                                                                                                     LGIDYPSIHYSNAI---SSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
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-QPSGNPFDQSSQPQQQPQQ-QPAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
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APPLICATION NUMBER:
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APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
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APPLICANT: Town, Christine
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                                       381
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 239 LTTGMDVYTNVDQEA----
                                                                      184 KNQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNL 238
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                    QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI 438
                                                                                                            DNEIRGFPLASLYYFGRPVEELSLDQQALLVGMVKGASIYNPWRNPKLALERRNLVLRLL 380
                                                                                                                                              SNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEM 183
                                                                                                                                                                                   GASTLTAALVKNLFLS----SERSYWRKANEAYMALIMDARYSKDRILELYMNEVYLGQSG 320
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                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0,
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TELEFAX: (212) 354-811
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                     APPLICATION NUMBER: IN 5
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New Yor
                                                                                                           REGISTRATION NUMBER: 35,372
                                                                                                                                                                                       APPLICATION NUMBER:
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                                                     TELEPHONE:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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US-08-481-435-9
; Sequence 9, Application US/08481435
; Patent No. 6027906
; GENERAL INFORMATION:
; APPLICANT: Balganesh, Tanjore S
; APPLICANT: Town, Christine
; TITLE OF INVENTION: No. 6027906e1
; NUMBER OF SEQUENCES: 42
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US-08-481-435-8
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Best Local S
Matches 201
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNLQS-NSLQ
                                                                                                                                                                                              SEMQQ-----QPSGNPFDQSSQPQQQPQQ-QPAQ
                                                                                                                                                                                                                             SSTSQSSSTTPSTUNSTTTNPNNNTQQSUTTPDQQNQNPQPAQ
                                                                                                                                                                                                                                                                                                                                 ----NNV-----DTWFAGIDGSTVTITWVGRDNN-QPTKLYGASGAMSIYQ---RY
                                                                                                                                                                                                                                                                                                                                                                   DEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTTGMDVYTNVDQEA-------QKHLWDIYNTDEYVAYPDDELQVASTIVDVS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNL
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                                                                                                                                                                                                                                                                LA-NQTPTPLNLVPPEDIADMGVDYDGNFVCSGGMRILPVWTS----
                                                                                                                                                                                                                                                                                                 LSEGSNPEDWNI--PE----GLYRNGEFVFKNGAR--STWNSPAPQQPPSTESSSSSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGVPKDQLHPVPAMLLGALNLTPIE------VAQAFQTIASGGNRAPLSALRSVIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGIDYPSIHYSNAI---SSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APIALRQPNGQVWSPQNDDRRYSESGRVMLVDALTRSMNVPTVNLGMALGLPAVTETWIK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPYNYPGTNTPVY---NWDRGY--FGNITLQYALQQSRNVPAVETLNKYGLNRAKTFLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTT----FDSVAQDAAEKAAVEGIPALKKQRKLSD-------LETAIVVVDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI 438
                                                                                                                                                                                                                                                                                                                                                                                                     DGKVLYQSFPQ-AERAVPAQAAYLTLWTMQQVVQRGTGRQLGAKYPNLHLAGKTGTTN--
   No. 6027906el Polypeptides: 42
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US-08-481-435-9
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Best Local Similarity
Matches 197; Conserv
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APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 819-87
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
ORGANISM: ESC
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OPERATING SYSTEM: PC-DY
SOFTWARE: PatentIn Rela
CURRENT APPLICATION DATA:
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CLONE: pARC046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                            261 ----TVQLVKNLFLS---SERSYWRKANEAYMALIMDARYSKDRILELYMNEVYLGQSGD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 MISSPNGEQRLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGR--- 260
                                                                                                                                                                                                                                                                                                                                                                                                                  69
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REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995
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                  PYNYPGTNTPVY---NWDRGY--FGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGL
                                                                                               GKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDE 344
                                                                                                                                                                          TTGMDVYTNVDQEA------QKHLWDIYNTDEYVAYPDDELQVASTIVDVSN 285
                                                                                                                                                                                                                                                                                              NEIRGFPLASLYYFGRPVEELSLDQQALLVGMVKGASIYNPWRNPKLALERRNLVLRLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNLQSNSLQG
                                                      GEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIADA
                                                                                                                                      TT----FDSVAQDAAEKAAVEGIPALKKQRKLSD
                                                                                                                                                                                                                 QQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKIF
                                                                                                                                                                                                                                                    NQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNLL
                                                                                                                                                                                                                                                                                                                                     NGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMK 184
                                                                                                                                                                                                                                                                                                                                                                                                              GSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYM----S
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version
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US-08-245-511-24
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Masure, H
APPLICANT: Pearce, Ba
APPLICANT: Tuomanen,
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                            TELEPHONE: 201 487-5800
                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                           HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERCE/DOCKET NUMBER: 600-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                  ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NNV-----DTWFAGIDGSTVTITWVGRDNN-QPTKLYGASGAMSIYQ---RYL
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R6
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Pearce, Barbara J
                                                                                                                                      unknown
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                Streptococcus pneumoniae
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                                                        N-terminal
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                                                                                                                 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24,
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Best Local
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                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Masure, H ROBERT
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Ellainen
APPLICANT: Tuomanen,
                          FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Str
                                                                                                                                                                                                                                                                                                               FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                           MOLECULE TYPE: PO
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 NVSFGINQAVETNRDWG
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                                                                                                                                                                                                     TELEPHONE: 201 30.
                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/
FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NVSFGINQAVETNRDWG
                                                                                                                            TOPOLOGY:
                                                                                                                                                        LENGTH:
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77; Conserv
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5981229
                                                                                                                                         amino acid
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                                                                                                                                                     77 amino acids
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Pearce, Barbara J
                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klauber & Jackson
                                                           N-terminal
                                                                                                        peptide
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                US 08/116,541
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Pred. No. 6.2e-24;
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US-08-481-435-12
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US-08-600-993A-24
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Best Local Similarity
Thes 77; Conserve
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Query Match
Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                   TELEFAX: (212) 354-81
                                                                                                       IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: IN 580/MAS/9.
FILING DATE: 01-7UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Reluction Data:
                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: White & Case
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Balganesh, Tanjore S APPLICANT: Town, Christine
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                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                      amino acid
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(212) 35،
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States
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Conservative
         Conservative
                                                                                                                              Escherichia coli
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          linear
                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                354-8113
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                     10.6%; Score 370.5; DB 3; 30.7%; Pred. No. 6.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 406; DB 2; 100.0%; Pred. No. 6.2e-24; ive 0; Mismatches 0;
                                                                                                truncated soluble PBP
                                                                                                                                                                                                                                                                                                                                                                                                                               IN 580/MAS/94
       68;
                                                                                                                                                                                                                                                                                                             1103326-151
       Mismatches
       138;
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                                     Length 532;
       Indels
       53;
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      Gaps
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       12;
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US-08-481-435-11
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                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: 10-JUL-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                TELEPHONE: (212) 819-8783
                                                                                                                                                                                                              FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: IN 51 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: SE 9.
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: NO. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 MISSPNGEQRLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                             NAME: Sterner, Richard J. REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTT----FDSVAQDAAEKAAVEGIPALKKQRKLSD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIAD 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTTGMDVYTNVDQEA------QKHLWDIYNTDEYVAYPDDELQVASTIVDVS 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, Application US/08481435
6027906
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10036-2787
                    amino acid
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                                      553 amino acids
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1155 Avenue of the Americas
                                                                                                  (212) 354-8113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/481,435
10-JUL-1995
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; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; IMMEDIATE SOURCE:
; CLONE: parc 0592 truncated PBP 1B
US-08-481-435-11
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                                                                                                                              439 FTT----FDSVAQDAAEKAAVEGIPALKKQRKLSD------LETAIVVVDRF 480
                                                                                                                                                                                                                                                             536 APIALROPNGOVWS 549
                                                                 481
                                                                                        285 NGKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHD 343
                                                                                                                                                                                             381 QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI 438
                                                                                                                                                                                                                                                                                                                               344 EPYNYPGTNTPVYN 357
                                                                                                                                                     239 LTTGMDVYTNVDQEA-------QKHLWDIYNTDEYVAYPDDELQVASTIVDVS 284
                                                                                                                                                                                                                184 KNQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNL 238
                                                                                                                                                                                                                                                                                                                                                                                               204 MISSPNGEORLEVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                    SGEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIAD 535
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Search completed: June 13, 2002, 08:41:58 Job time: 84 sec

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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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    Pending_Patents_AA_Main:*
|: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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2032.241 Million cell updates/sec
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3484
              /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
/cgn2_6/ptodata/2/paa/US087_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3466	3466	3483	3483	3484	3484	3484	Score
99.5	99.5	100.0	100.0	100.0	100.0	100.0	Query Match
719	719	721	719	666	666	666	Query Match Length DB
22	ш	15	19	21	21	19	BB
US-09-815-242-13423	PCT-US02-03987-13423	US-09-107-433-3705	US-09-583-110-3973	US-09-765-272-2	US-09-765-271-2	0S-09-536-784-2	ID
Sequence 13423, A	Sequence 13423, A	Sequence 3705, Ap	Sequence 3973, Ap	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Description

## ALIGNMENTS

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US-09-536-784-2
US-09-536-784-2

Sequence 2, Application US/09536784

GENERAL INFORMATION:
APPLICANT: CNoi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION UNMBER: 08/961,083
FILING DATE: OCT-30-197
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: PB340P3
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RESULT 2
US-09-765-271-2
; Sequence 2, Application US/09765271
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptocor
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-81 TELEFAX: (301) 309-81 TELEFAX: EQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                        661
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                       PQPAQP
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                                                                                                                                                 AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
                                                                                                                                                                                                                                                 MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM
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TYPE: amino acid
STRANDEDNESS: single
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Streptococcus
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Pred. No. 3e-289;
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                  pneumoniae
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
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Best Local S
Matches 666
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                                     VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                                                                                               TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                                          SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                                                                 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                             GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                      VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                                                                 TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                            SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                                                     VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                              666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Scient
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09, FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
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Pred. No. 3e-289;
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US-09-765-272-2
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                                                                                                                         Query Match
Best Local Similarity
                                                                                                           Matches 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09765272
                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID -09-765-272-2
                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-850
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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61 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                      1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/961,083
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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ADDRESSEE: Human Genome Sciences, Inc.
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                                    KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
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                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001
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                                                                                                                                                                                                                                                   TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue
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                                                                                                           Conservative
                                                                                                     100.0%; Score 3484; DB 2
100.0%; Pred. No. 3e-289;
tive 0; Mismatches (
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1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN

Matches 665; Best Local Similarity

Conservative

1;

Pred. No. 4.2e-289; 1; Mismatches 0; Score 3483;

Indels Length

0;

Gaps

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DB 19;

Query Match

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US-09-583-110-3973; Sequence 3973, Application US/09583110; GENERAL INFORMATION:
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                                                                ; ORGANISM: Streptococcus pneumoniae US-09-583-110-3973
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                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 3973
LENGTH: 719
TYPE: PRT
                                                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02
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RESULT 5
US-09-107-433-3705
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
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COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   714
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                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS
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                                                                                                                                              STREET: 100 Beaver St. CITY: Waltham STATE: Massachusetts COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 3705:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
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FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051853
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                             KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
                                                                                                                                                                                                                     VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                                                                                                                                                                                                                                                                                         TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
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 STWNSPAPQQPPSTESSSSSSSSSTSQSSSTTPSTNUSTTTNPNNNTQQSNTTPDQQNQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 235
                                                                                                                                                                                                                                                                                VSFGINQAVETNRDWGSTMKPITDYAPALEYGIYDSTATIVHDEPYNYPGTNTPVYNWDR
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99.8%;
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TITLE OF INVENTION: Methods for Identifying the Tai TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITERA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER: 60/267
NUMBER: FastSEQ for Windows Version 4.0
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 719
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APPLICANT: Elitra Pharmaceuticals, Inc.
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                                                                                   MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM 540
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                             AVWTGYSNRLTPLYGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR 600
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                                                                                                                                                                                                   GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
  STWNSPAPQQPPSTESSSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
                                                                                                                                           KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 533
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Pred. No. 1.2e-287;
Mismatches 1; Indels
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US-09-815-242-13423
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13423
LENGTH: 719
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APPLICANT: Ohlsen, K:
APPLICANT: Zyskind,
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                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                 Conservative
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/255,625 PRIOR APPLICATION NUMBER: 60/255 PRIOR APPLICATION NUMBER: 60/255 PRIOR APPLICATION PRIOR PRIOR APPLICATION NUMBER: 60/255 PRIOR APPLICATION PRIOR PRIOR APPLICATION PRIOR PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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                                                                     TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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Pred. No. 1.2e-287;
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PRIOR APPLICATION NUMBER: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 13423
LENGTH: 719
PYPER: FOR THE PRIOR OF THE PRIO
                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptococcus
US-10-072-851-13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-072-851-13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13423, Application US/10072851
GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT EPPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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                                                                                 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
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                                                                                                                                                                         662;
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Jiang, Bo
Boone, Charles
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Yamamoto, Robert T.
Roemer, Terry
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Zyskind, Judith W.
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                                                                                                                                                                         Score 3466; DB 24;
Pred. No. 1.2e-287;
3; Mismatches 1;
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US-09-107-532-5667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5667, Application US/09107532 GENERAL INFORMATION:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0515
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ENTEROCOCCUS FABCIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7308
                                                                                                                                                                                               SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME TH
  ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Be CITY: Waltham
                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                    100 Beaver Street
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                                          60/051571
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TELECOMMUNICATION INFORMATION:

NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-0

GTC-012

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781)893-827
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: misc_feature LOCATION: 1...823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: PIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: YOURGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
                                                                                                                                                                                                                                                          -KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT 479
                                                                                                                                                                                                                                                                                                                    GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD 420
                                                                                                                                                                                                                                                                                                                                                                                  VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                           DGLEIYTNLDLDAQKKLYDIVNTDQYVSYPDDEMQVASTLIDTNTGKVKAQIGGRHIAED 414
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTMLQNEKISQTEYDQAVNVPVTDGLQELTQSDDNTKIVDNYVKEVINEVQEKTDKNVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLYTQDGELFEDLGAEKREKISANELPKTLEDAIVSVEDRRFYKHIGVDPIRIIGSALSN 174
                          --TTNPNNNTQQSNT----TPDQQNQNP
                                                                                                                                                MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYR-NGEFVFKN- 597
                                                                                                                                                                              DILKDTITEGTGTNAQIAGLYQAGKTGTSNYTDDEYAK-LGISSGYYPDILFAGYTPNYS
                                                                                                                                                                                                                                          GTKYGASSLKMAAAYAAFANGGTYYKPQYVNKIVFQDGTEETYEPDGKTAMSPETAYMIT
                                                                                                                                                                                                                                                                                                    QYMGTITLRQALYLSRNVPAVKLFNEVGSDKVASFLKNLGIEYSTIHQSNAISSNTEEQD
                                                                                                                                                                                                                                                                                                                                                                VTLGNNLAVNTSRDFGSTMKPVTDYGPAFEYLKY-STGKTITDAPYNYEGTSTPVGNWDN 473
                                                          YTARSNAITPSTTIPSSSYVQTPGSSTTETTTQSSSSTSQSESTAESSKESTTAETSEPA
                                                                                                                                                                                                            DMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYS 539
SSTTVPSSSSEESSTPSSSAPPASSSEP
                                                                                       -GARSTWNSPAPOQP------PSTESSSSSSDSSTSQSSSTTPSTNNST-----
                                                                                                                   ISVWTGYNKKMTPVTSESSHVASDVYRELMQYVSANVTNTDWEMPSGLIRVGGELYYKDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-8277
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53.9%;
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RESULT 10
US-09-107-532A-5667
; Sequence 5667, Application US/09107532A
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
; APPLICANT: Lynn A DOUCETTE ACID
TITLE OF INVENTION: NUCLEIC ACID
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Best Local :
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                                                        181 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
                                                                                                                                  175
                                                                                                                                                                                                                                                                   295 YTMLQNEKISQTEYDQAVNVPVTDGLQELTQSDDNTKIVDNYVKEVINEVQEKTDKNVYT
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APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                         1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                             LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                              VYMSNGLYGMETASEMYFGKKLSELSLPQTALLAGMPQAPSAYDPYVYPDQAKKRRDTVL
                                                                                                                                                                                         FTSGGLQGGSTLTQQLIKLSFFSTSAEDQTLKRKAQEAWMAVRLEQKKSKQEILTYYVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 823 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/107,532A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING
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                                                                                                                                                                                                                                                                                                                                              Conservative 109; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  53.5%;
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                                                                                                                                                                                                                                                                                                                                                                  Score 1862.5; DB Pred. No. 7e-150;
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                179; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                    Length 823;
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300
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PCT-USO2-03987-10728

Sequence 10728, Application PC/TUS0203987

GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Enterococcus faecalis PCT-US02-03987-10728
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 10728
LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US02/03987 CURRENT FILING DATE: 2002-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                               1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
                                                                                                                                                                                                                                                     SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                              VKNGGLQGGSTLTQQLIKLSYFSTKESDQTLKRKAQEAWMAVRLEREKSKEEILTYYINK
                                                                                                                                                                                          LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --TTNPNNNTQQSNT----TPDQQNQNP 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTKYGASSLKMAAAYAAFANGGTYYKPQYVNKIVFQDGTEETYEPDGKTAMSPETAYMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYMGTITLRQALYLSRNVPAVKLFNEVGSDKVASFLKNLGIEYSTIHQSNAISSNTEEQD
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YTMYDNKKISKAEYEKAKATPIDEGLVPLKASDDNRKVVDNYVKEVINEVKAKTGKNVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLGNNLAVNTSRDFGSTMKPVTDYGPAFEYLKY-STGKTITDAPYNYEGTSTPVGNWDN
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          50.3%; Score 1751; DB 1; 51.4%; Pred. No. 2.4e-140;
                                                                                                                                                                                                                                                                                                                                      125;
                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                Length 778;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/11,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10728
LENGTH: 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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RESULT 13
US-10-072-851-10728
Sequence 10728, Application US/10072851
GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Foulkes, J. Gordon
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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INVENTION:
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347; Conser
                                                                                                                                                       Trawick, John D. Yamamoto, Robert
                                                                                                                                                                                                               Wall, Daniel
                                                                        Jiang, Bo
Boone, Charles
                                                                                                                                 Roemer,
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Methods for Identifying
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Pred. No. 2.4e-140;
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                            Inhibits
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; FILE REFERENCE: ELITRA.028A; CURRENT APPLICATION NUMBER: US/10/072,85; CURRENT FILING DATE: 2002-02-08; PRIOR APPLICATION NUMBER: 60/267,636; PRIOR FILING DATE: 2001-02-09; NUMBER OF SEQ ID NOS: 15811; SOFTWARE: FastSEQ for Windows Version 4.; SEQ ID NO 10728; LENGTH: 778
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SSAEQPATSEQPPEP
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                       TTPDQQNQNPQPAQP 666
                                                   YEVPNVQVLPSTTSSAPQPESSSTVESSSTKEAESSSSSSSSSAPSSSEAPPSTEQPASS
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US-09-134-000-4939
, Sequence 4939, Application US/09134000A
; GENERAL INFORMATION:
, APPLICAMT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AN

NUCLEIC ACID AND AMINO

ACID

SEQUENCES

RELATING

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RESULT 15
US-08-116-541-4
US-08-116-541-4
; Sequence 4, Application US/08116541
; GENERAL INFORMATION:

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US-09-134-000-4939
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CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 4939
LENGTH: 789
TYPE: PRT
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Best Local Similarity
Matches 347; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INV
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               Toumanen,
                            Masure, H. Robert
Pearce, Barbara J.
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 BACTERIAL EXPORTED
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; MOLECULE TYPE:
US-08-116-541-4
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Best Local (
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack Avenue STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/116,
FILING DATE: 19930901
CLASSIFICATION: 424
ATTORNEY_AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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305
                           301
                                                       245
                                                                                  241
                                                                                                              185
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                                                                                                                                        181
                                                                                                                                                                    125
                                                                                                                                                                                               121
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                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
              VSFGINQAVETNRDWG
                                                                      TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                           SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                         LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
VSFGINQAVETNRDWG
                                                      TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                            SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                    VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 amino acids
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99.7%;
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320
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Pred. No. 7.2e-130
                                                                                                                                                                                                                                                                                                                                          Mismatches
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completed: June 13, ne: 248 sec

2002,

08:44:42

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being parand is derived by analysis of the total score distribution.
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BB
   3484
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526
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160.52
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141.131.55
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seq length: 2000000000
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3484
1 KIYDNKNQLIADL
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Com
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              US-09-673-605A-34
US-09-442-489B-2
US-09-914-543-10
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US-09-987-482-1
US-09-987-482-1
US-09-935-625-7547
US-09-935-625-7546
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US-09-540-209B-9358
US-09-914-543-6
US-09-882-227-522
US-09-882-227-408
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US-09-540-209B-6592
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US-09-769-744A-122
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Sequence 122, App
Sequence 8941, App
Sequence 9358, App
Sequence 622, Appli
Sequence 522, App
Sequence 408, Appli
Sequence 3, Appli
Sequence 6592, App
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ALIGNMENTS	US-09-540-209B-9400	US-60-360-039-2471	US-60-360-039-15126	US-60-360-039-14653	US-60-360-039-14305	US-60-360-039-22177	US-60-360-039-22288	US-09-200-650D-7	US-60-360-039-7473	US-60-360-039-4713	US-60-360-039-1535	US-09-540-209B-10169	US-09-540-209B-6575	US-09-935-625-29528	US-09-935-625-8783	US-09-935-625-29529	US-09-935-625-8784	US-09-935-625-28206	US-09-935-625-7548	
	Sequence 9400, Ap	2471,			Sequence 14305, A					4713,	1535,	10169,	6575,	29528,	8783,	29529,	8784,	28206,	Sequence 7548, Ap	
	ALIGNMENTS	5 US-09-540-209B-9400 Sequence 9400, ALIGNMENTS	123 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 122 3.5 648 5 US-09-540-209B-9400 Sequence 9400, ALIGNMENTS	124 3.6 889 7 US-60-360-039-15126 Sequence 15126, 123 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 122 3.5 648 5 US-09-540-209B-9400 Sequence 9400, ALIGNMENTS	124 3.6 889 7 US-60-360-039-14653 Sequence 14653, 124 3.6 889 7 US-60-360-039-15126 Sequence 15126, 123 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 122 3.5 648 5 US-09-540-209B-9400 Sequence 9400, ALIGNMENTS	124 3.6 889 7 US-60-360-039-14305 Sequence 14305, 124 3.6 889 7 US-60-360-039-14653 Sequence 14653, 124 3.6 889 7 US-60-360-039-15126 Sequence 15126, 123 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 122 3.5 648 5 US-09-540-209B-9400 Sequence 9400, ALIGNMENTS	124 3.6 650 7 US-60-360-039-22177 Sequence 22177, 124 3.6 889 7 US-60-360-039-14535 Sequence 14305, 124 3.6 889 7 US-60-360-039-14653 Sequence 14653, 124 3.6 889 7 US-60-360-039-15126 Sequence 14653, 124 3.6 889 7 US-60-360-039-15126 Sequence 15126, 123 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 122 3.5 648 5 US-09-540-209B-9400 Sequence 9400, 125 3.5 648 5 US-09-540-209B-9400	124.5 3.6 1169 7 US-60-360-039-22288 Sequence 124 3.6 650 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-14305 Sequence 124 3.6 889 7 US-60-360-039-14653 Sequence 124 3.6 889 7 US-60-360-039-15126 Sequence 123 3.5 1504 7 US-60-360-039-2471 Sequence 123 3.5 648 5 US-09-540-209B-9400 Sequence 126 3.5 648 5 US-09-540-209B-9400	125 3.6 1166 5 US-09-200-650D-7 Sequence 124.5 3.6 1197 US-60-360-039-22288 Sequence 124 3.6 650 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-14305 Sequence 124 3.6 889 7 US-60-360-039-14505 Sequence 124 3.6 889 7 US-60-360-039-14526 Sequence 123 3.5 1504 7 US-60-360-039-2471 Sequence 122 3.5 648 5 US-09-540-209B-9400 Sequence 126 3.5 648 5 US-09-540-209B-9400 Sequence	125 3.6 655 7 US-60-360-039-7473 Sequence 7473, 125 3.6 1166 5 US-09-200-650D-7 Sequence 7, App 124.5 3.6 1169 7 US-60-360-039-22288 Sequence 22288, 124 3.6 650 7 US-60-360-039-22177 Sequence 22217, 124 3.6 889 7 US-60-360-039-14653 Sequence 14305, 124 3.6 889 7 US-60-360-039-14653 Sequence 14305, 124 3.6 889 7 US-60-360-039-14653 Sequence 14305, 124 3.6 889 7 US-60-360-039-15126 Sequence 15126, 125 3.5 1504 7 US-60-360-039-2471 Sequence 2471, 127 3.5 648 5 US-09-540-209B-9400 Sequence 9400, 128 ALIGNMENTS	125 3.6 655 7 US-60-360-039-4713 Sequence 125 3.6 1165 5 US-09-300-639-7473 Sequence 125 3.6 1166 5 US-09-200-650D-7 Sequence 124.5 3.6 1169 7 US-60-360-039-22288 Sequence 124 3.6 650 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-14305 Sequence 124 3.6 889 7 US-60-360-039-1453 Sequence 124 3.6 889 7 US-60-360-039-1453 Sequence 124 3.6 889 7 US-60-360-039-15126 Sequence 125 3.5 1504 7 US-60-360-039-2471 Sequence 127 3.5 648 5 US-09-540-209B-9400 Sequence	127.5 3.7 1609 7 US-60-360-039-1535 Sequence 125 3.6 655 7 US-60-360-039-4713 Sequence 125 3.6 655 7 US-60-360-039-4713 Sequence 125 3.6 1166 5 US-09-200-650D-7 124 3.6 1169 7 US-60-360-039-22288 Sequence 124 3.6 650 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-14305 Sequence 124 3.6 889 7 US-60-360-039-14503 Sequence 124 3.6 889 7 US-60-360-039-14526 Sequence 124 3.6 889 7 US-60-360-039-1526 Sequence 125 3.5 1504 7 US-60-360-039-2471 Sequence 126 Sequence 127 3.5 648 5 US-09-540-209B-9400 Sequence	128 3.7 1029 5 US-09-540-209B-10169 Sequence 127.5 3.7 1609 7 US-60-360-039-1535 Sequence 125 3.6 655 7 US-60-360-039-4713 Sequence 125 3.6 655 7 US-60-360-039-4713 Sequence 124.5 3.6 1166 5 US-09-200-650D-7 124.5 3.6 1169 7 US-60-360-039-22288 Sequence 124.5 3.6 1169 7 US-60-360-039-22177 Sequence 124.5 3.6 889 7 US-60-360-039-22177 Sequence 124.5 3.6 889 7 US-60-360-039-14305 Sequence 124.5 3.6 889 7 US-60-360-039-1453 Sequence 124.5 3.6 889 7 US-60-360-039-1453 Sequence 124.5 3.6 889 7 US-60-360-039-15126 Sequence 125 3.5 1504 7 US-60-360-039-2471 Sequence 126 3.5 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1043 5 US-09-935-625-29529 Sequence 131 3.8 1043 5 US-09-935-625-29528 Sequence 132 3.8 1043 5 US-09-935-625-29528 Sequence 123 3.8 1043 5 US-09-940-209B-6575 Sequence 124 3.6 655 7 US-09-540-209B-610169 Sequence 125 3.6 655 7 US-60-360-039-135 Sequence 125 3.6 655 7 US-60-360-039-4713 Sequence 125 3.6 655 7 US-60-360-039-22278 Sequence 124 3.6 650 7 US-60-360-039-22277 Sequence 124 3.6 650 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-1126 Sequence 124 3.6 889 7 US-60-360-039-1126 Sequence 124 3.6 889 7 US-60-360-039-15126 Sequence 125 3.5 1504 7 US-60-360-039-15126 Sequence 126 3.5 1504 7 US-60-360-039-2471 Sequence 127 3.5 648 5 US-09-540-209B-9400 Sequence	131 3.8 1031 5 US-09-935-625-8784 Sequence 131 3.8 1031 5 US-09-935-625-29529 Sequence 131 3.8 1043 5 US-09-935-625-29528 Sequence 131 3.8 1043 5 US-09-935-625-29528 Sequence 132 3.8 1043 5 US-09-935-625-29528 Sequence 123 3.7 1609 5 US-09-540-209B-575 Sequence 124 3.7 1609 7 US-60-360-039-1535 Sequence 125 3.6 655 7 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Sequence 124 3.6 889 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-2177 Sequence 125 3.6 1169 7 US-60-360-039-2177 Sequence 126 3.6 889 7 US-60-360-039-15126 Sequence 127 3.5 889 7 US-60-360-039-15126 Sequence 128 3.5 1504 7 US-60-360-039-2471 Sequence 129 3.5 648 5 US-09-540-209B-9400 Sequence 120 3.5 648 5 US-09-540-209B-9400 Sequence	131 3.8 989 5 US-09-935-625-7548 Sequence 131 3.8 1031 5 US-09-935-625-28206 Sequence 131 3.8 1031 5 US-09-935-625-8794 Sequence 131 3.8 1031 5 US-09-935-625-28529 Sequence 131 3.8 1043 5 US-09-935-625-8783 Sequence 131 3.8 1043 5 US-09-935-625-8783 Sequence 129 3.7 1043 5 US-09-540-209B-10169 Sequence 129 3.7 1609 7 US-60-360-039-1535 Sequence 127.5 3.6 655 7 US-60-360-039-7473 Sequence 125 3.6 655 7 US-60-360-039-7473 Sequence 124.5 3.6 1169 7 US-60-360-039-22288 Sequence 124.5 3.6 1169 7 US-60-360-039-2277 Sequence 124 3.6 889 7 US-60-360-039-22177 Sequence 124 3.6 889 7 US-60-360-039-14535 Sequence 124 3.6 889 7 US-60-360-039-14535 Sequence 124 3.6 889 7 US-60-360-039-1516 Sequence 125 3.5 1504 7 US-60-360-039-1516 Sequence 126 3.5 1504 7 US-60-360-039-2471 Sequence 127 3.5 648 5 US-09-540-209B-9400 Sequence 128 3.5 1504 7 US-60-360-039-2471 Sequence 129 3.5 648 5 US-09-540-209B-9400 Sequence

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TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCEDESCRIPTION: SEQUENC
Query Match
Best Local Similarity
Matches 666; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
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FILING DATE: 30-OCT-1997
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 666 amino acids
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                                           Score 3484; DB 4; Pred. No. 1.7e-217;
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Mismatches

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Indels

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Gaps

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Conservative

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FILE REFERENCE: PWC/P21122WO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR PLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 122
LENGTH: 821
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US-09-769-744A-122
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                                                                                                                                                                                                                                                                 Sequence 122, Application US/09769744A GENERAL INFORMATION:
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APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
                          TYPE: PRT
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Sequence 8941, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Berton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 8941
LENGTH: 789
TYPE: PRT
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Best Local Sim
Matches 203;
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APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9358
LENGTH: 790
TYPE: PRT
ORGANISM: B.fragilis
                                                                                                                                                                                        RESULT 4
US-09-540-209B-9358
; Sequence 9358, Application US/09540209B
; GENERAL INFORMATION:
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US-09-540-209B-8941
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-09-540-209B-9358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYGRRQVGSTIKDYL-YALAMENGFSPCDETRNVEITLIDENGKPWSPKNT----SKGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VETNRDWGSTMKPITDYAPALEYGV--YDST----ATIVHDEPYNYPGTNTPVYNWDRGY 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLTQQLIKLTYFSTSTSDQTISRKAQE--AW-LAIQLEQKATKQEILTYYINKYYMSNGN 127
                                                                                                                                                                                                                                                                                                                                                                                                                         MMKTVLTYGTGRNA--YLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKY 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ISVGEMVSAYTAFANKGIRVAPLFVTKIEDSEGNVLATFSPQMEEVISASSAYKMLV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGEMVTLKWGLANSNNWISAYLMSKLNPYALARLIHSFGVRNKEIQPTVSLCLGPCE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGN-ITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDK 421
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                                                                                                                                                                                                                                                                                                                                                   SMAVWTGYSNR----LTPLVGNGLTVAAKVYRSMM--TYLSE--GSNP-EDWNIPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFTWHGVKDTIMSPMDSIRYYKHFLRAGFMSMDPINGQVKAYVGGPNYT---YFQYDMA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YISAEQYEKAVNTPI-----TDGL------QSLKSASNYPAY-MDNYLK 224
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; LENGTH: 875
; TYPE: PRT
; ORGANISM: Bankia ;
US-09-914-543-6
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US-09-914-543-6
; Sequence 6, Application US/09914543
; GENERAL INFORMATION:
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                                                                                                                                            APPLICANT: DIVERSA CORPORATION
APPLICANT: MATHUR, ETIC
TITLE OF INVENTION: ENDOGLUCANASES
FILE REFERENCE: DIVERII50-5
CURRENT APPLICATION UNMBER: US/09/914,543
CURRENT FILING DATE: 1998-11-22
PRIOR APPLICATION NUMBER: PCT/US97/08793
PRIOR APPLICATION NUMBER: US/09/914,543
PRIOR APPLICATION NUMBER: US/08/651,572
PRIOR APPLICATION NUMBER: US/08/651,572
PRIOR APPLICATION NUMBER: US/08/651,572
PRIOR APPLICATION NUMBER: US/08/651,572
PRIOR FILING DATE: 1996-05-22
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                                                                                   NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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hes 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLVLSEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHI 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPV 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSVSTIDRGIQTQIESLVER--WN----SEFKR--SDIRNLAILVIDIRTNQAIAYCGNV
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36; Conservative
                    gouldi
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```

Query Match
Best Local Similarity

4.6%; 21.1%;

Score Pred.

162; DB 5; No. 0.015;

Conservative

Mismatches

196;

Indels

178;

26;

Qy

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APPLICANT: Miller, Charles

APPLICANT: Tomb, Jean-Francois

APPLICANT: Ocomen, Raymond P.

TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding Novel Helicobacter Polypept
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002

CURRENT APPLICATION NUMBER: US/09/882,227

CURRENT APPLICATION NUMBER: US/09/882,227

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US/09/882,227

NUMBER OF SEQ ID NOS: 638

NUMBER OF SEQ ID NOS: 638
                                                                                                                               ; ORGANISM: Helicobacter US-09-882-227-522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-882-227-522
                   Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 522
LENGTH: 2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 522, Application US/09882227 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles
                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRFYEMKAVIQNH-STTPAQGKDDLYMRYFYDLSEVFAAGYSLNDLTVASGYNQASDVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPAYMDNYLKEVINQVEEETGYNLLTTGMD-VYTNVDQEAQKHLWDIYNTDEYVAYPDDE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVDSSLTYGIDAPKIPLYDANGL--LWGEEPPRGGTSSSSSSSSSSSSSSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETTAYMMTDMMKTVLTYGTG-RNAYLAWLPQAGKTGTSNYTDEE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVNQRHVLYG-----AVAGGPQGDTGYEEDRNDYVQNEVATD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTTESDKKYGASSEKMAAAYAAFANGGTYY---KPMYIHKVVFSDGSEKEFSNVGTRAMK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIGSDHPLYDRYHNFGKKQIDHILGDNPDNQSYVVGFGDNFPINVHHRGSHGSWSDSISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQSRNVPAVETLNKVGLNRA------KTFLNGLGIDYP-SIH-----YSNAISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVLMAALVGDEVYHADAQRYLDHWSVGEGNRTPNGLILVDSWGVNRYAANAGYLALFYAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAATLITHAKQLWQFADSTKG----TTGTDTAYSNCITGAQG----FYTSTYGVY-YDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQHWDGNVYYVEAQFYDDVVFPGGQSAHRREVQFRVSLPTTSNLAEWDNTNDPSFDPSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAWGALWLWRATGEDFYLEQAKHYYGLMGFE-NQTTTPVYTWSLGW----NDKA----YAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IENHIKTSQFVAPDELFAGYTRKYSMAVWTGYS-NRLTPLVG-----NG
                              Conservative 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VAAKVYRSMM----
                                                                                                                                                                                                                                                                                                                                                                                                   Encoding Novel Helicobacter Polypeptides in the Helicobacter
                         4.6%; Score 160.5; DB 5; 19.5%; Pred. No. 0.098; tive 103; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YNSGFTSAVAALYDHYGGAPLANFPPPEPESVEYLVGAKINSSG
                                                                                                                                                  pylori
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                                                                Length
                            Indels
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                            35;
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 408
                                                                                                                                                                                                                                                                      US-09-882-227-408
; Sequence 408, Application US/09882227
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
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                                                                                                                                                                   APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding Novel Helicobacter Polyn
TITLE OF INVENTION: Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AISSNTTESDKKYGASSEKMAAAYAAFANGGTYYKP-----MYIH--KVVFS-DGS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YINADMPWYDHKYYIPKSQ-----NFTESGTYYLPSVQIWGSYTNSFKQTFSANGSNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFGSSKITLAQGTTFNLTSLGSEKSVTILNSSGGITYSNLLNHAINGLTSALKTNESLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NGARSTWNSPAPQQPPSTESSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYSAYHVYI-TANLRSGNRIGTG------GAAN----LIFNGVDSINIANATITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGL-----TVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGYNSTWTDHNVSSSGTVSFGDTS------GSALNGHCGPWPYYQCTGTTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EKEFSNYGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T---IYKLQETFSHNSIIIQALESGTYTP------PPVINGSKFD---LSASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNTPVYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSN 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQSFAQGLWDIITYNGVTGQLLNENAATSKP-TDSSPSKS----STNSTQVYQVGYKIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----W------GSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVSNGKV------IAQLGAR-----HQSSNVSF-----GINQAVETNRD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYS---HPEAAQDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDN
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Helicobacter

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US-09-200-650D-3
; Sequence 3, Application US/09200650D
; GENERAL INFORMATION:
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TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-408
                                                                                                                                                                            US-09-200-650D-3
                                                                                                                                                                                                                                                                  FILE REFERENCE: P06283US2/BAS
CURRENT APPLICATION NUMBER: US/09/200,65
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,815
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: 60/098,427
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 22
                                                                                           Query Match 4.4%; Score 153.5; DI Best Local Similarity 20.4%; Pred. No. 0.058; Matches 155; Conservative 96; Mismatches 7
                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.6%;
Best Local Similarity 21.5%;
Matches 84; Conservative 64
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hook, Magnus A.O.
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Foster, Timothy J. APPLICANT: Eidhinn, Deirdre N. APPLICANT: Hook, Magnus A.O. APPLICANT: Perkins, Samuel L.
                                                                                                                                                                                    TYPE: PRT
ORGANISM: Staphylococcus
                                                                                                                                                                                                                          LENGTH: 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 GYVQKQEEDKLT---LTTGKKGVEKS----QDHLLKAQQNGIRTGKRDVSFNFIQNHS
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                               80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLGAR------HQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTAT
NKVY--MSNGNYGMQTAAQNY-YGKDLNNL-----SLPQLAL--LAGMPQAPNQYD 164
                             RQLKDNT----QTATADQPKVTMSDSATVKETSSN-----MQSPQNATANQSTTKTS
                                                           RNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LIKVVRYGTGKNAQFEGLYIGGKTGTA 531
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Pred. No. 0.014;
P4; Mismatches 125; Indels 1
                                                                                                                         DB 5;
                                                                                            288;
                                                                                            Indels 221;
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                                                                                                                                      ; SEQ ID NO 6592
; LENGTH: 188
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-6592
                                                                                                                                                                                                                                                                                                                  US-09-540-209B-6592
, Sequence 6592, Application US/09540209B; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
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                                                           Query Match
Best Local Similarity
Matches 48; Conserv
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4
EDGAFYFHRGFLPEAMRKALYQDLKVKRFARGGSTITMQLVKSVFLS---RNKNIARKLE
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                                                           Conservative
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CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1001-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 DS-STSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 NKDGKRDSTEKGIKGVKVTLQNEKGEVIGTTETDENGKYR--FDNLDSGKYKVIFEKPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 PAGYTPTTANVG----TDDAVDSDGLTTTGVIKDADNMTLDSGFYKTPKYSLGDYVWYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 GKQDANEKGIKGVY---VILKDSNGKELDRTTT---DENGKYQFTGLSNG--TYSVEFST
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                                  EDHRFFDHRGIDTIRILGAFLRNLQ-SNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYRNG-----EFVFKNG--ARSTWNSPAPQQPPSTESSSSSS 621
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                                                                                                     4.2%; Score 148; DB 5;
27.6%; Pred. No. 0.014;
tive 34; Mismatches 76
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                                                                                                        76;
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                                                                                                                                                             Length 188;
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US-09-673-605A-34
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SEQ ID NO 34
LENGTH: 595
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Best Local Similarity 22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The President and Fellows of Harvard College TITLE OF INVENTION: REGULATION OF BIOFILM FORMATION FILE REFERENCE: 00246/505003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/673,605A CURRENT FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/102,870
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/083,259
PRIOR FILING DATE: 1998-04-27
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                  RAKTFLNGL---GIDYPSIHYSN--AISSNTTESDKKYGASSEKMAAAYAAFANGGTYYK 445
                                                                                                                                                                                                                                                                                                            YDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITL---QYALQQSRNVPAVETLNKVGLN 390
                                                                                                                                                                                                                                                                                                                                                                                                                            LNGFNVNGSGTIANKAATISDLTAAKMDAATNT-----ITTTNNALTASKALDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIKGLTQAARNANDGI-SVAQTTEGALSEINN-NLQRIRELT--VQASTGTNSDSDLDSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTNSL---SLITQNNINKNQSALSSSIERLS-----SGLRINSAKDDAAGQAIANRFTS
                                        GTASAKYADNTDVSNATATYTDADGEMTTIGSYTTKYSIDANNGKVTVDSGTGSGKYAPK
                                                                            KTGTSNYTDEEIENHIKTSQFVAPDEL--FAGYTRKYSMAVWTGY-----SNRLTPL
                                                                                                                                                                                              TAAT-LDGLFKKAGDGQSIGFNKTASVTMGGTTYNFKTGAD----AGAATANAG----
                                                                                                                                                                                                                                                                                                                                                  KDGDTVTIKADAAQTATVYTYNASAGNFSFS-NVSNNTSAKAGDVAASLLPPAGQTASGV
                                                                                                                                                                                                                                                                                                                                                                                        QVASTIVDVSNGKVIAQLGARHQSS-NVSFGINQAVETNRDWGSTMKPITDYAPALEYGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGMPQAPNQY-----DPYSHPEAAQDRRNLVLSEMKNQGYIS---AEQYEKAVN 199
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  VGNGLTVAAKVYRSMMTYL---
                                                                                                                                                        PMYIHKVVFSDGSEKE--FSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAG
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                                                                                                                  -VSFTDTASKETVLNKVAT--AKQGTAVAANGDTSATITYKSGVQTYQAVFAAGD
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                                                                                                                                                                                                                                                                          ----NFDVDANGKITIGGQEAYLTSDGNL----TINDAGGA 319
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  --SEGSNPED--WNIPEGLYRNGEFVFKNGARSTWNSP 606
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SOFTMARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2843
TYPE: PRT
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Best Local Similarity
Matches 130; Conserv
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CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: US 08/452,654
PRIOR FILING DATE: 1995-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: White, Raymond L. TITLE OF INVENTION: APC Antibodies FILE REFERENCE: 001107.78817
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                   LNKVGLN-----RAKTFLNGLGID-----
                                                                                                                                                                                                                                                                                                                                                            KALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYV---
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                                                        ERNALR----RSSAAHTHSNTYNF----TKSENSNR----TCSMPYAKLEYKRS--SNDS
                                                                                         YAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA-LQQSRNVPAVET
                                                                                                                                GTSSKRGLQISTTAAQIA - - KVMEEVSAIHTS
                                                                                                                                                                   -----LQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGST--MKPITD 324
                                                                                                                                                                                                            RGSLDSSRSEKDRSLERERG----TGLGNY-----
                                                                                                                                                                                                                                                                                  ---FDTNRHDDNRSDNFNTGNMTVLSPY------LNTTV-----LPSSSSS
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Groden, Joanna
Hedge, Philip John
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Vogelstein, Bert
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18.8%; Pred. No. 0.83;
tive 98; Mismatches 213
               ----YPS----IHYSNAISSNTTESDK 421
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Sequence 10, Application US/09914543
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: LAM, David
APPLICANT: MATHUR, ETIC
TITLE OF INVENTION: ENDOGLUCANASES
FILE REFERENCE: DIVER1150-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10
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CURRENT FILING DATE: 1998-11-22
PRIOR APPLICATION NUMBER: PCT/US97/08793
PRIOR FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: US 08/651,572
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                               123 MSNGNYGMQTAAQNYYG-----KDLNNLSLPQLALLAGMPQA--PNQYDPYSHPEAAQ 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 GLYRNGEFVFKNGARSTWNSP-----APQQPPSTESSSSSSSDSSTSQSSSTT-PSTNN 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           964 LNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDT
                                                                              ---IAY-----TLHFYAGTHGSWLRDKARNAMNSGIALFVT-----EWG-TVNADG 264
                                                                                                                                                                                                                                                                                        ARVRALVDAAIAEDMYVIIDFHTHHAEDYQ-----AESIEFFEEMATLYGGY-DNVIY 163
                                                                                                                                                                                                                                                                                                                                           DR-RNLVLSEMKNQGYI-----SAEQYEKAVNTPITDGLQSLKS-ASNYPAYMDNYLK 224
                                                                                                                              DEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPIT
                                                                                                                                                                                                                                                                                                                                                                                            WSNTGWGQ----ERFYNAETVRWLKDDWNATIVRAAMGVDFDGSYIPEHED--ADPEGNV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLMIKSTLTGMITAVAAAVFTTSAAFADVPP-----LTVSGNQVLSGGEAKSFAGNSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLQGGSTLTQQL--IKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVY 122
                                                                                                                                                                                    EIYNEPLQISWDNVIKPYAESVIGAIRAIDPDNLIIVGTPTWSQDVDAAARNPITSYSN-
                                                                                                                                                                                                                                  EVINQ-------VEEETGY------NLLTTGMDVYT-NVDQEAQKHLWDIYNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PINYSLKY--SDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRN-----QSTT 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERPTNYSTKYNEEKRHV-DQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 143; DB 5; Length 1010; llarity 19.5%; Pred. No. 0.31; Conservative 111; Mismatches 285; Indels 14
                             -----LEYGVYDST--ATIVHDEPYNYPGTNTPVYNWDRGYF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YTESTDDKHLKFQPHFGQQECVSPYR 1103
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US-09-442-489B-7
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APPLICANT: Vogelstein, Bert
APPLICANT: White, Raymond L.
TITLE OF INVENTION: APC Antibodies
FILE REFERENCE: 001107.78817
CURRENT APPLICATION NUMBER: US/09/442,489B
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: US 08/452,654
PRIOR FILING DATE: 1995-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 154
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                          Query Match 4.0%; Score 141; DB 5; Best Local Similarity 18.7%; Pred. No. 1.8; Matches 129; Conservative 99; Mismatches 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09442489B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 07/741,940 PRIOR FILING DATE: 1991-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/289,548 PRIOR FILING DATE: 1994-08-12
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                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2842
TYPE: PRT
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                                                                                                      723 AALRNLMANRPAKYKDANIMSPGSSLPSLHVR--
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                                                                                                                                                    56 AFLRNLQSNS-----LQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQ 106
KALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYV----
                                                   KATKQEILTYYINKVYMSNGNY------GMQTAAQNYYGKDLNNLSLPQLALLAGMPQA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS---DGSEKEFSNVGTRAMKETTAYMMT 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNG- 598
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Hedge, Philip John
Joslyn, Geoff
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                                                                                                                                                                                                            213;
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ORGANISM: Teredinibacter

LENGTH: 1010 TYPE: PRT

Best Local Similarity Matches 131; Conserv

Query Match Best Local :

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SEQUENCE 1, Application US/09987482

GENERAL INFORMATION:
APPLICANT: BHANDARI, POONAM
APPLICANT: SHASHIDHARA, L.S.
TITLE OF INVENTION: IN VIVO ASSAY SYSTEM FOR SCREENING AND TITLE OF INVENTION: DRUGS AND OTHER SUBSTANCES
FILE REFERENCE: 058659-0134
CURRENT APPLICATION NUMBER: US/09/987,482
CURRENT FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2843
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-482-1
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US-09-987-482-1
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Best Local Similarity
Matches 129; Conserv
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                                                                                724 AALRNLMANRPAKYKDANIMSPGSSLPSLHVR------
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                                                                                                                 56 AFLRNLQSNS-----LQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STTTNPNNNTQQSN----TTPDQQNQNPQPA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERPTNYSIKYNEEKRHV-DQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSS 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYRNGEFVFKNGARSTWNSP-----APQQPPSTESSSSSSSSSTSQSSSTT-PSTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SR-----GANGSETURVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHEEE 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PINYSLKY--SDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRN-----QSTT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERNALR----RSSAAHTHSNTYNF----TKSENSNR----TCSMPYAKLEYKRS--SNDS 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA-LQQSRNVPAVET 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTSSKRGLQISTTAAQIA--KVMEEVSAIHTS-----QEDRSSGSTTELHCVTD 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGSLDSSRSEKDRSLERERG----IGLGNY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAYMDNYLKEVINQVEEETGYNLLTTGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---FDTNRHDDNRSDNFNTGNMTVLSPY------LNTTV-----LPSSSSS
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KALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMM-----TYLSEGSNPEDWNIPE 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGST--MKPITD
                                                                                                                                                           Conservative
                                                                                                                                                         4.0%; Score 141; DB 5; Length 2843;
18.7%; Pred. No. 1.8;
rative 99; Mismatches 213; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- HPATENP 869
                                                                                                                                                           Indels 250;
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                                                                             ------KQ 757
                                                                                                                                                           Gaps
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800
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	150	ΩL	LNNLSLPQ	AQNYYGKD	AWLAIQLEQKATKQEILTYYINKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQL-	YYINKVYI	KQEILT	AIQLEQKAT,	EAWL	97	Qy
	55	ASGLSTAE	DDTSLVRNASG	IIPCPS	SSSTTGDGYAPS		LSLAAD	LQASSLISG	LRNI	ω	Ъ
	9	AQ	DQTISRK-		STSTS	LIKLTYF	STLTQQ	LRN-LQSNSLQGGSTLTQQLIKLTYFSTSTS	LRN-	58	Ωу
40;	Gaps	06; 279;	Length 7 Indels	DB 7; 2; 227;	Score 139.5; Pred. No. 0.32 ; Mismatches	; Sco ; Pre	4.0% 19.0% vative	ch l Similarity 146; Conservat	cat	Query M Best Lo Matches	Z m O
					ë	cerevisia		TYPE: PRT ORGANISM: Saccharomyces 0-360-039-1865	PRT  ISM:  -039-	TYPE: ORGAN 60-360	S
						4	: 4/3/	65 ID NOS	NO 1865	NUMBER O	ξΩ.
					/360,039	2)A : US/60/360, -02-21	0(5205 NUMBER 2002	E REFERENCE: 38-10(52052)A REENT APPLICATION NUMBER: US/ REENT FILING DATE: 2002-02-21	EFERE T APP	FILE RE CURRENT CURRENT	
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					0039	us/6036003	ion	0 × 0 H	15 360-039- 360-186 ence 186 RAL INFO LICANT:	ESULT 15 S-60-360-039 Sequence 18 GENERAL INE APPLICANT:	
					2PQKA 1246	SAQSRSG	NQLHPS	ENTSTPSSNAKRQNQLHPSSAQSRSGQPQKA		1216	ф
					NPQPA 664	TTPDQQNQNPQPA	NT	STTTNPNNNTQQSN-		638	Qy
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	585	PEDWNIPE	TYLSEGSNPEDWNIPE	T	3 :	GNGLTVAJ  : :	RLTPLV	RKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMM- :           :   : : CDCANGGETMADVGSNHGTNONVGOSTOO		536	P 29
	1103	:   )ECVSPYR	<b>FQPHFGQQ</b>		YTE				YPV-	1075	Db
	535	DELFAGYT	TSQFVAPE	EEIENHIK	YMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYT	YLAWLPQ	GTGRNA	DMMKTVLTY		476	QΥ
		::  QSTT	QSRN	:: EIKQSEQR	SDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRN-	: : QSPSQNEI	:: : QLNSGR			1024	Db :
	475	RAMKETTA	EFSNVGTR	VESDGSEK	KYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTA	AAFANGG	KMAAAY	KYGASSE		2	0
	1023	ONDGELDT	IHISNAISSNITESDR    :  :       IHSANHMDDNDGELDT	QYPADLAHKI	YGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDT	IESYSEDI	GQMKPSIESYS	g :		964	₽ 5
		RS SNDS	TCSMPYAKLEYKRS	TCSM	-TKSENSN	1 1	-RSSAAHTHSNTYNF-	1		918	Ъ
		RNVPAVET	YFGNITLQYA-LQQSRNVPAVET	YFGNITLO	YAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRG	EPYNYPG:	ATIVHD	:   IEYGVYDST		325	Qy
	917	FELHCVTD	-QEDRSSGSTTELHCVTD	1	SAIHTS	-KVMEEVSAIHTS	-AAQIA	SSKRGLQISTTAAQIA	GT	871	Db
	324	MKPITD	NRDWGST-	GINQAVET	LQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGST-	GKVIAQLO	IVDVSN	LQVAST	1	274	Qy
	870	:    -HPATENP		1	IGLGNY	GI(	:    SLERER	: :   :		838	Db
	273	AYPDDE	YNTDEYVA	'AQKHLWDI	PAYMDNYLKEVINQVEEETGYNLLTTGMDVYTNVDQEAQKHLMDIYNTDEYVAYPDDE	GYNLLTT	QVEEET	IDNYLKEVIN		216	Qy
	837	-LPSSSSS	LUTTY	CIEKAVNI	NUGITSAB	GNMTVLS	SDNENT	EDTINHEDDNRSDNENTGNMTVLSPY-		801	Db 45
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¥	255	KHLWDIYNTDEYVAYPDDELQVA-STIVDVSNGKVIAQLGAR
ğ	212	SDAGFNISLSDLWARALSYNF FPSLPDAGSALTWSSLRDVDVFKNGEMPLPITVADGR
γ	296	HQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNT
ğ	270	
Qy	354	PYYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYP
Db	313	GKPV-NKDQCVSGYDNAGFVIATSASLFNEFSLEASTSTYYKMINSFANKYVNNLSQDDD 371
Qy	405	SI
Db	372	   DIAIYAANPFKDTEFVDRNYTSSIVDADDLFLVDGGEDGQNLPLVPLIKKERDLDVVFAL 431
Qy	412	-ISSNTTESDKKYGASSEKMAAAYAAFANGGTYYKDMYI
Вþ	432	DISDNTDESWPSGVCMTNTYERQYSKQGKGMAFPYVPDVNTFLNLGLTNKPTFFGCDAKN 491
Qy	450	HKVVFSDGSEKEFS-NVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLP 500
В	492	LTDLEYIPPLVVYIPNTKHSFNGNQSTLKMNYNVTERLGMIRNGF
Qy	501	QAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRL 550
DЪ	537	EAATMGNFTDDSNFLGCIGCAIIRRKQESINATLPPECTKCFADYCWNG
Qy	551	TPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQ 610
Db	586	LSGNSTYQSGAIASAISEATDG 616
Qy	611	PPSTESSSSSDSTSQSSSTTPSTNNSTTTNPNNNTQQSN 651
뮹	617	IPITALLGSSTSGNTTSNSTTSTSSNVTSNSNSSSNTTLNSNSSSSS 663

Search completed: June 13, 2002, 08:41:39 Job time: 65 sec

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Result
No.
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Maximum DB
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Streptococcus pneu Streptococcus pneu Streptococcus pneu Enterococcus faeca S. pneumoniae deri Streptococcus pneu Streptococcus pneu Drosophila melanog N-terminal truncat
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S. pneumoniae peni
Streptococcus pneu
Streptococcus pneu
Streptococcus pneu
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Sequence of Heliot	AAR49657	15	1704	1.5	10	30
Haemophilus influe	AAU35684	22	781	1.5	10	29
Pseudomonas aerugi	AAU36453	22	774	1.5	10	28
Streptococcus pneu	AAY81653	21	694	1.5	10	27
Choline binding pr	AAY32099	20	655	1.5	10	26
CbpA of serotype 4	AAY49226	20	655	1.5	10	25
Group B Streptococ	AAU03646	22	462	1.5	10	24
N-terminal choline	AAY32189	20	460	1.5	10	23
N-terminal region	AAY49250	20	460	1.5	10	22
N-terminal choline	AAY32190	20	459	1.5	10	21
N-terminal region	AAY49251	20	459	1.5	10	20
Amino acid sequenc	AAY49143	20	446	1.5	10	19
Amino acid sequenc	AAY49140	20	446	1.5	10	18
C glutamicum prote	AAG92949	22	438	1.5	10	17
Choline binding pr	AAY32110	20	428	1.5	10	16
Choline binding pr	AAY49238	20	428	1.5	10	15
Choline binding pr	AAY32098	20	406	1.5	10	14
Polypeptide R2 of	AAY49225	20	406	1.5	10	13
Choline binding pr	AAY32100	20	284	1.5	10	12

## ALIGNMENTS

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AAW55063
                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                          WPI; 1998-272224/24.
N-PSDB; AAV27323.
                                                                                                                                            Choi GH, Hromockyj A, Johnson LS, Kunsch
                                                                                                                                                                                               07-MAY-1998.
                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                    Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                   02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                             AAW55063 standard; Protein; 666
                                                                                                                                                                      31-OCT-1996;
                                                                                                                                                                                   30-OCT-1997;
                                                                                                                                                                                                            W09818930-A2
                                                                                                                                                                                                                                                                                 AAW55063;
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                        pneumoniae.
                                                                                                                                                                                                                                                      pneumoniae SP001 protein.
                                                                                                                                                                      96US-0029960
                                                                                                                                                                                   97WO-US19422
                                                                                                                                                                                                                                                                                             A
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Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis

Claim 11; Page 48; 118pp; English.

The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, orally or through the skin, typically at 0.01-1000

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RESULT
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ID AAWO
XX AAWO
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XX AAWO
XX O3-U
DT 03-U
XX S. F
XX Peni
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            Penicillin binding protein; PBP 1A; bifutransglycosylase; transpeptidase; identiantibiotic resistant; bacteria; soluble
                          Penicillin
                                                       03-DEC-1996
                                                                    AAW04359;
                                                                                  AAW04359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  666;
       crystallography;
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                                                                                 standard;
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                                        penicillin
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            1A; bifunctional p
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soluble variant; p
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                                        protein 1A soluble variant
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                   l protein;
n; assay;
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             structure;
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                    inhibitor;
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Matches 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sol. derivs. of bifunctional penicillin binding opt. lack transglycosylase activity, useful to i for antibodies or cpds. which bind BPBPs
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          crystallography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Balganesh TS,
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01-JUL-1994;
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                    NRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
                                                                                                                                                           EAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVET
                                                                                                                                                                                                      TAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYISA
RNAYLAWLPQAGKTGTSNYTDEETENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLT
                                                                                                              nrdwgstmkpitdyapaleygvyestativhdepynypgtntpvynwdrgyfgnitlqya
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                                                                                                                                                                                                                                                    taaqnyygkdlnnlslpqlallagmpqapnqydpyshpeaaqdrrnlvlsemknqgyisa
                                                                                                                                                                                                                                                                                                ltqqlikltyfststsdqtisrkaqeawlaiqleqkatkqeiltyyinkvymsngnygmq
                                                                                                                                                                                                                                                                                                                                             530;
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94IN-0000580
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99.6%;
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                                               The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antiblotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                       Note: The sequence unclaim of the printed specification, but format directly from WIPO at format directly from blished_pct_seq
                                                                                                                                                                                                                                                                                                                                New polynucleotides for antibiotics, comprise
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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Yamamoto RT,
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Sequence
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16-FEB-2001;
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                        int/pub/published_pct_sequences
719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotic cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial;
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penicillin binding penicillin vaccine;
WPI; 1995-115448/15
N-PSDB; AAQ83241.
                                                 01-SEP-1993;
18-MAY-1994;
                                                                                    09-MAR-1995
                                                                                                 W09506732-A2
                                                                                                                                          Exp2; export protein; pbpla; plpA; exp1; exp3;
virulence determinant; permease like protein;
                                                                                                                                                                Streptococcus
                                                                                                                                                                              14-FEB-1996
                                                                                                                                                                                                          AAR70153 standard;
                      Masure HR,
                                   (UYRQ ) UNIV
                                                                      01-SEP-1994;
                                                                                                               Streptococcus
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                     Pearce BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                   ROCKEFELLER
                                                                                                                                                                              (first
                                                                                                                                                               pneumoniae strain SPRU42 Exp2
                                                                                                               pneumoniae
                                                 93US-0116541.
94US-0245511.
                                                                      94WO-US09942
                                                                                                                            nant; permease like protein;
protein lA; pyruvate oxida
antibody.
                                                                                                                                                                                                           Protein;
                                                                                                                                                                              entry)
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                      Tuomanen
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Pred. No. 0;
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                                                                                                                                     oxidase; regulatory
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Matches 245; Conserv
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                                                                                                                                                     05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transpeptidase encoding re detection; identification;
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(SAME-) SOUTH
                                                                               01-AUG-1997;
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Pred. No. 1e-233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and identifying any antibiotic-resistant s. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be used to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of s. pneumoniae with a minimum inhibitory concentration (MIC) of 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and 24 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate protein concentration (TER) isolate protein
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DB; AAZ35939.
                                                                         LAWLPQAGKTGTSNYTDEEIENHIKTSQEVAPDELFAGYTRKYSMAVWTGYSNRLTPLVG
                                                                                                                                 AFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAY
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                                                         lawlpqagktgtsnytdeeienhiktsqfvapdelfagytrkysmavwtgysnrltplvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n assays for detecting Streptococcus of pneumococcal meningitis
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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic for mat directly from WIPO at
                                                                                                                                                              Query Match
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Matches 14
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
              AAY86004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3;
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Yamamoto RT,
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22-DEC-2000;
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23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic cellular proliferation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis cellular proliferation protein #422
                                        AAY86004 standard; Protein;
                                                                                                                                                                                                                                                             itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2000;
                                                                                                            146
                                                                                                                                      66 LQGGSTLTQQLIKL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-611495/70.
                                                                                                           lgggstltgglikl 159
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC
                                                                                                                                                                                                                                     778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
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2000US-257931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen
Xu HH;
                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID No 10728; 511pp; English.
                                                                                                                                                              2.1%; Score 14; DB
100.0%; Pred. No. 0.1
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug
                                        266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          design.
                                                                                                                                                                           DB 22;
. 0.0001;
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                                                                                                                                                                                        Length 778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · 6
                                                                                                                                                              0;
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                                                                                                                                                              Gaps
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                                                                                                                                                                                                        RESULT
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Query Match
Best Local s
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-Z96494) and their encoded proteins (see AAZ965792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics.
Streptococcus pneumoniae
                               pneumococcal septicaemia;
                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 493-494; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae proteins and related DNA screening compounds for antibacterial activity % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2000
                                                  bacterial pneumonia; asplikidney disease; diabetes;
                                                                                   Streptococcus
                                                                                                                                                   02-JUN-2000
                                                                                                                                                                                  AAY81757;
                                                                                                                                                                                                                   AAY81757 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ96344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-159452/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09806734-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     They are also useful to determine their infection, dysfunction and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-1996;
                                                                                                                                                                                                                                                                                                   107 ggstltgglik 117
                                                                                                                                                                                                                                                                                                                                    68 GGSTLTQQLIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae derived
                                                                                                                                                                                                                                                                                                                                                                   Similarity 100
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevention; disease; diagnosis; gene therapy; screening;
antimicrobial; antibiotic; pathogenesis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                 (first entry)
                                                                pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
umonia; asplenia; heart disease; lung disease; alcoholism;
                                                                                                                pneumoniae protein sequence ID113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                   1.7%; Score 11; DB
100.0%; Pred. No. 0.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles
                                sinusitis;
                                              enia; heart disease; lung disease; alcohol immunosuppressive disorder; otitis media;
                                                                                                                                                                                                                   821
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                                                                                                                                                                                                                   AA
                                meningitis; therapy
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                                                                                                                                                                                                                                                                                                                                                                                  DB 19;
0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     role in pathogenesis
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or diagnostic of S. pneumoniae infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
 31-OCT-1996;
                           30-OCT-1997;
                                                       07-MAY-1998
                                                                                                             Streptococcus
                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                        detection;
                                                                                                                                                       Streptococcus pneumoniae; antigen; vaccine; infection;
                                                                                                                                                                                                              02-OCT-1998
                                                                                                                                                                                                                                        AAW55113;
                                                                                                                                                                                                                                                                  AAW55113 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments)are useful as immunogens or antigens. Immunogenic or antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcal proteins and polynucleotides useful treatment and prophylaxis of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ91853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                                                                                                                                 68 GGSTLTQQLIK 78
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                                                                                                                                                                                                                                                                                                                                       ggstltgglik 186
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                        pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                 pneumoniae SP0062 protein.
                                                                                                             pneumoniae
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96US-0029960
                           97WO-US19422
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99US-0125329
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                                                                                                                                                                                                                                                                                                                                                                                      1.7%; 5u-
100.0%; Pr
                                                                                                                                        otitis
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                                                                                                                                                                                                                                                                                                                                                                                           Score 11; DB
s; Pred. No. 0.1
0; Mismatches
                                                                                                                                                                                                                                                                  110
                                                                                                                                        media;
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                                                                                                                                          meningitis
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0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic or antigenic
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                                                                                                                                                     diagnosis;
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ABB69173
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific monitoring infections. Antibodies which bind the protein are used to detect specific antibodies in standard immunoassays, especially for diagnosing or their content corresponding antipodies which bind the protein are used to detect specific antipodies. Antibodies which bind the protein are used to detect corresponding antipodies which bind the protein are used to detect the content of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-272224/24.
N-PSDB; AAV27374.
                                             N-PSDB; ABL13276
                                                                    WPI; 2001-656860/75
                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 34311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB69173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                               (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a protein from Streptococcus pneumoniae nucleic acid sequence encoding the Streptococcus pneumoniae protein
                                                                                                                                                                    CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AA;
                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                    2000US-191637P
2000US-0614150
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                                                                                                                       PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                       Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunsch CA;
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0.15;
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New isolated nucleic acid detection reagent for detecting 1000 or more

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL161840-ABL16175) and the encoded proteins The sequence 3.4--
The invention provides novel isolated polypeptides comprising the amino acid sequence of an N-terminal choline binding protein A (CbpA) truncate (CbpAY). The polypeptides can be selected from sequences shown in AAY49225, AAY49227, AAY49230, AAY49231, AAY49233 and AAY49238. The polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. The can also be used for preventing infection by a pneumococcal bacterium. Vaccines comprising the polypeptides or encoding nucleic acids can be
                                                                                                       Novel polypeptides, used to develop products for the prevention and treatment of pneumococcal infections
                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                               Choline binding protein A; CbpA; pneumococcal bacterium; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                      N-PSDB;
                                                                                                                                              WPI; 1999-620161/53.
                                                                                                                                                                                                       07-APR-1998;
07-APR-1998;
                                                                                                                                                                                                                                                                                                                                         N-terminal truncate of CbpA serotype type 4 polypeptide R1
                                                                                                                                                                                                                                                                                                                                                              07-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                  AAY49227 standard; Protein; 284
                                                                                        Claim
                                                                                                                                                                                                                                    07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617
                                                                                                                                                                                                                                                                                                                                                                                                                                                60 sssssdssts 69
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                                                                                      3; Page 11; 85pp; English.
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                                                                                                                                                                  Masure
                                                                                                                                                                                                                                                                                           pneumoniae
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98US-0080878
                                                                                                                                                                                                                                    99WO-US07668
                                                                                                                                                                                    CHILDREN'S
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                                                                                                                                                                                     RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10;
Pred. No.
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                                                                                                                                                                                     HOSPITAL
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                                                                                                                                                                                                                                                                                                                        truncate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Listing; English
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0.17;
                                                                                                                                                                                                                                                                                                                       immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                  diagnosis
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                                                           truncate
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AAY32100
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               The present sequence represents polypeptide R1, a new N-terminal choline binding protein A (CbpA) truncate derived from the CbpA of Streptococcus pneumoniae serotype type 4. Host-vector systems for production of R1 and other CbpA truncated polypeptides are provided. The invention relates generally to novel N-terminal CbpA truncates and polynucleotides encoding them, host-vector systems, and antibodies that specifically bind to the polypeptides. The invention also relates to vaccines including CbpA polypeptides, which provide protection or elicit protective antibodies to bacterial infection, specifically penumococcus, and to use of
                                                                                                                                                                                                                                                                                                                                                                             New N-terminal choline binding protein A truncate polypeptides, develop products for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuomanen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1998;
07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choline binding protein; CbpA; truncate; adhesin; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium. Antibódies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment to a mucosal surface. The products can be used in humans and other animals such as domestic animals, such as feline or canine subjects, farm animals
                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otitis media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choline binding protein A (CbpA) truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY32100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 10;
Local Similarity 100.0%; Pred. No.
hes 10; Conservative 0; Mismato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EI,
                                                                                                                                                                                                                                                                                                        Page 93-95; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masure HR,
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98US-0080878.
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                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumococcus; sepsis; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOSPITAL
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polypeptides
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0.37;
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Best Local S
Matches 10
                            vaccines comprising the polypeptides or encoding nucleic acids can be used for treating a subject infected with or exposed to a pneumococcal bacterium. Antibodies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment t a mucosal surface. The products can be used in humans and other animals such as domestic animals, such as feline or cannine subjects, farm animal such as bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research animals, such as mice, rats, rabbits, goats, sheep, pigs, dogs, cats, i.e. for veterinary medical use.
                                                                                                                                                                             The invention provides novel isolated polypeptides comprising the amino acid sequence of an N-terminal choline binding protein A (CbpA) truncate (CbpAT). The polypeptides can be selected from sequences shown in ANY49225, ANY49227, ANY49230, ANY49231, ANY49233 and ANY49238. The polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. The can also be used for preventing infection by a pneumococcal bacterium.
Sequence
                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                     prevention
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-620161/53
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07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choline binding protein A; CbpA; truncate; immune response; infection; pneumococcal bacterium; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and passive immunotherapy. The polypeptides and/or polynucleotides are also useful as competitive inhibitors of bacterial adhesin of pneumococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide R2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                    polypeptides, used 
ntion and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                       Page 7-8;
   406 AA
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98US-0080878.
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                                                                                                                                                                                                                                                                                                                                    to develop products for the diagnosis of pneumococcal infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    b; Pred. No. 0.3
0; Mismatches
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0.37;
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                                                                                                                                                                                                                                                           truncate
                                                                                        animals
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AAY32098
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                                                               The present sequence represents polypeptide R2, a new N-terminal choline binding protein A (CDpA) truncate of Streptococcus pneumoniae serotype type 4. Host-vector systems for production of R2 and other N-terminal CDpA truncates are provided. Important features of R2 include: (1) complete correlation of bioactivity with full-length CDpA for recognition of purified glycoconjugate receptor analogues, ung cells and animal models; and (2) cross-protection between type 4 derived agents and bacteria in in vitro assays using other serotypes (e.g. 6B and 2), important for use in vaccine, prophylaxis and therapy. The invention relates generally to novel N-terminal CDpA truncates and polynucleotides encoding them, host-vector systems, and antibodies that specifically bind to the truncates. The invention also relates to vaccines including N-terminal CDpA truncates, which provide protection or elicit protective antibodies to bacterial infection, specifically pneumococcus, and to use of antibodies and antagonists against such polypeptides in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                               New N-terminal choline binding protedevelop products for the diagnosis, pneumococcal infections
Sequence
                                          and passive immunotherapy. The are also useful as competitive
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-633690/54.
N-PSDB; AAZ34451.
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07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choline binding protein; CbpA; truncate; adhesin; vaccine; diagnosis; therapy; pneumococcus; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choline binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2000
                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 85-88; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL. (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EI,
 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0056019
98US-0080878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US07669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein A (CbpA) truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy; pneumococcus; sepsis; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wizemann TM, Johnson LS,
                                          The polypeptides and/or polynucleotides ive inhibitors of bacterial adhesin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               protein A truncate polypeptides, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koenig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,:
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Query Match

Score 10;

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                                                                                                            Query Match
Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides novel isolated polypeptides comprising the amino acid sequence of an N-terminal choline binding protein A (CbpA) truncate (CbpAT). The polypeptides can be selected from sequences shown in AAY49227, AAY49227, AAY49230, AAY49231, AAY49233 and AAY49238 The polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choline binding protein A; CbpA; pneumococcal bacterium; vaccine.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                               animals,
                                                                                                                                                                                                                                                                            such as bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research
                                                                                                                                                                                                                                                                                                           Vaccines comprising the polypeptides or encoding nucleic acids can be used for treating a subject infected with or exposed to a pneumococcal bacterium. Antibodies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment to a mucosal surface. The products can be used in humans and other animals such as domestic animals, such as feline or canine subjects, farm animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1998;
07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choline binding protein A (CbpA) serotype type 4 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49238 standard;
                                                                                                                                                                                                                                          1.e.
                                                                                                                                                                                                                                                                                                                                                                                                                            can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-620161/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuomanen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SJUD-) ST JUDE CHILDREN'S RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2000
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                                                                       616
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                                                                                                                               Local Similarity
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                                    sssssdsst 122
                                                                       SSSSSSDSST 625
                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSSSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides, used ntion and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EI,
                                                                                                                                                                                                                                          veterinary medical use.
                                                                                                                                                                                                                                                           such as mice, rats, rabbits,
                                                                                                                                                                                                     428 AA;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0056019
98US-0080878
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                                                                                                                                                                                                                                                                                                                                                                                                                          for preventing infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 428
                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; CbpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to develop products for the diagnosis, of pneumococcal infections -
                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                             Score 10;
Pred. No.
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                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 truncate;
                                                                                                                                                                                                                                                           goats, sheep,
                                                                                                                           DB 20;
0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
                                                                                                                                                                                                                                                                                                                                                                                                                            a pneumococcal bacterium.
                                                                                                            0;
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                                                                                                                                             Length 428
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                           pigs,
                                                                                                            0,
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                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             They
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AAY3
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AC AA
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AAG92949
ID AAG929
DX AC X
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                                  AAG92949;
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                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuomanen EI,
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07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                   428
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RESULT
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      The invention also relates to vaccines including N-terminal CbpA truncates, which provide protection or elicit protective antibodies to bacterial infection, specifically pneumococcus, and to use of antibodies and antagonists against such polypeptides in diagnosis and passive immunotherapy. The polypeptides and/or polynucleotides are also useful as competitive inhibitors of bacterial adhesin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; diagnosis;
otitis media; pneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choline binding protein A (CbpA) N-terminal truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32110 standard; Protein; 428
AAG92949 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CbpA truncates and polynucleotides encoding them, host-vector systems, and antibodies that specifically bind to the truncates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae serotype type 4 CbpA native protein. Host-vector systems for production of N-terminal CbpA truncates are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a new N-terminal choline binding protein A (CbpA) truncate that maintains the tertiary structure \alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 119-122; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumococcal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New N-terminal choline binding protein A truncate polypeptides, develop products for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-633690/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choline binding protein; CbpA; truncate;
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                                                                                                                113 sssssdsst 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates generally to novel N-terminal
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumonia.
                                                                                                                                                                                                                                                                                                                          AA;
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98US-0080878
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Protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; pneumococcus; sepsis; meningitis;
                                                                                                                                                                                                                               1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wizemann
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                                                                                                                                                                                                                                 Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                                                                                                                                 DB 20
0.54;
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                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                     Length 428
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                                                                                                                                                                                                            Indels
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Matches 10
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                      sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
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         Truncated surface binding protein; alpha helix; choline binding protein; vaccine; invasive bacterial infection; otitis media; sepsis; meningitis; lobar pneumonia infection; antibody; immature immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                              AAY49140;
                                                                                                                                     AAY49140 standard;
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tateishi
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                                                            Amino
                                                                                                                                                                                                                                                                                                                                                    specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK.
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Senoh A, Ikeda
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100.0%; O;
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Ozaki A;
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                                                                                                                                                                                                                                                                                                           The vaccine can be used for preventing (immunising) or treating invasive bacterial (especially pneumococcal) infections, especially otitis media (caused by S.pneumoniae), sepsis, meningitis and lobar pneumonia infections. Antibodies raised against the polypeptide are useful for detection, prevention (passive immunity) and treatment of S. pneumoniae infections. The vaccines are especially useful in immunocompromised patients, those with an immature immune system, or patients with an on
            AAY49143
                                                                                                                                                                                                                                                                   going pneumococcal infection. The vaccine avoids unnecessary expense an provides broad protection against a range of pneumococcal serotypes and it produces an improved and enhanced effect in preventing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New pneumococcal proteins pneumococcal infections -
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15-MAY-1998;
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                                       AAY49143
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10; Conserv
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                                       standard;
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                  going pneumococcal infection. The vaccine avoids unnecessary expense and provides broad protection against a range of pneumococcal serotypes and it produces an improved and enhanced effect in preventing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49137-Y49152 are amino acid sequences that are fragments of choline binding proteins (CBP). The fragments of the protein are the alpha helix forming parts of the CBPs from Streptococcus pneumoniae. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Truncated surface binding protein; alpha helix; choline binding
                07-FEB-2000
                                                AAY49251;
                                                                              AAY49251 standard;
                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumococcal infections
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15-MAY-1998;
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meningitis; lobar pneumonia infection; antibody; immature immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pneumococcal proteins useful as vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDIMMUNE INC.
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98US-0085743.
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                                                                              Protein;
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Streptococcus Synthetic.
                                                                                                                      Choline binding protein; CbpA; truncate; adhesin; immunogen; vaccine; diagnosis; therapy; pneumococcus; sepsis; meningiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as domestic animals, such as feline or canine subjects, farm a such as bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. They can also be used for preventing infection by a pneumococcal bacterium. Vaccines comprising the polypeptides or encoding nucleic acids can be used for treating a subject infected with or exposed to a pneumococcal bacterium. Antibodies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment to a mucosal surface. The products can be used in humans and other animals and contact the products can be used in humans and other animals.
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                                                                                                  otitis
                                                                                                                                                                                                                      N-terminal choline binding protein A (CbpA) truncate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides, used to develop products for the diagnosis, prevention and treatment of pneumococcal infections
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07-APR-1998;
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                                                                                                  media;
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                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                   RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                    Choline binding protein pneumococcal bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae CbpA. Claimed vaccines contain and N-terminal CbpA truncate such as the present sequence, or a polypeptide comprising a conserved region of the CbpA truncate. The vaccines provide protection or elicit protective antibodies to bacterial infection, specifically pneumococcus. Antibodies and and antagonists against the N-terminal CbpA truncates are used in
             Tuomanen EI,
                                                        07-APR-1998;
07-APR-1998;
                                                                                             07-APR-1999;
                                                                                                                    14-OCT-1999
                                                                                                                                         W09951187-A2
                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                      N-terminal region of CbpA polypeptide Ntype4.
                                                                                                                                                                                                                                               07-FEB-2000
                                                                                                                                                                                                                                                                      AAY49250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an N-terminal choline binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 47; Fig 2A-B; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New N-terminal choline binding protein A truncate polypeptides, develop products for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1998;
07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9951188-A2
                                                                                                                                                                                                                                                                                             AAY49250 standard; Protein; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuomanen EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL. (MEDI-) MEDIMMUNE INC.
                                 (SJUD-) ST JUDE CHILDREN'S RES
                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                            616 SSSSSSDSST 625
                                                                                                                                                                                                                                                                                                                                                      ssssssdsst 136
                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and passive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masure HR,
                                                                                                                                                               pneumoniae
                                                        98US-0056019.
98US-0080878.
                                                                                             99WO-US07668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0056019
98US-0080878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US07669
                                                                                                                                                                                                 protein A; CbpA; truncate; immune response;
                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Sc., 100.0%; Pr
                                                                                                                                                                                      vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wizemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             denoted ATCC4 CbpA trun, derived
                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                    HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TM,
                                                                                                                                                                                                                                                                                                                                                                                                             DB 20
0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koenig
                                                                                                                                                                                                 infection;
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AAY32189
ID AAY3
XX AAY3
AC AAY3
AC AAY3
AC CAO1
KW Chol
KW Chol
KW Chol
KW Chol
KW Chol
KW OTit
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OS Synt
XX W095
XX W0
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. They can also be used for preventing infection by a pneumococcal bacterium. Vaccines comprising the polypeptides or encoding nucleic acids can be used for treating a subject infected with or exposed to a pneumococcal bacterium. Antibodies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment to a mucosal surface. The products can be used in humans and other animals such as domestic animals, such as feline or canine subjects, farm animals such as bovine, equine, caprine, ovine, and porcine subjects, wild animals, such as mice, rats, rabbits, goats, sheep, pigs, dogs, cats, i.e. for veterinary medical use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choline binding protein; CbpA; truncate; adhesin; immunogen; vaccine; diagnosis; therapy; pneumococcus; sepsis; meningitis; otitis media; pneumonia.
                                                                                                                                                                                                                                                                                                                          07-APR-1998;
07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides novel isolated polypeptides comprising tracid sequence of an N-terminal choline binding protein A (CbpA) and the polypeptides can be selected from sequences shown AAY49225, AAY49227, AAY49230, AAY49231, AAY49233 and AAY49238.
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                    New N-terminal choline binding protein A truncate polypeptides, used to develop products for the diagnosis, prevention and treatment of
                                                                                                                   WPI; 1999-633690/54.
                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal choline binding protein A (CbpA) truncate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32189 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-620161/53
                                                                                                                                                                                                                              (SJUD-) ST JUDE CHILDREN'S RES (MEDI-) MEDIMMUNE INC.
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les 10; Conser
                                                                                                                                                                            EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                            Masure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae.
                                                                                                                                                                                                                                                                                                                          98US-0056019
98US-0080878
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US07669
                                                                                                                                                                            HR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85pp; English.
                                                                                                                                                                            Wizemann TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No.
                                                                                                                                                                                                                                                                  HOSPITAL
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0.57;
                                                                                                                                                                            Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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pneumococcal infections

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RESULT 24
AAU03646
       QΥ
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Best Local Similarity
Matches 10; Conser
AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus agalactiae) amino acid sequences of the invention. S. agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
                                                                                                                                                                                                          New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals
                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200132882-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group B Streptococcus; encapsulated bacterium; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group B Streptococcus antigenic protein, ID-122
                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                    Le Page RWF,
                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitis; neonate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU03646;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae CbpA. Claimed vaccines contain and N-terminal CbpA truncate such as the present sequence, or a polypeptide comprising a conserved region of the CbpA truncate.
                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 sssssdsst 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             616 SSSSSSDSST 625
                                                                                                                                                                                                                                                                                     2001-316444/33
                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polysaccharide vaccination.
                                                                                                                                                                                                                                                                       AAS07063
                                                                                                                                                                                 Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                  Μ̈́
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigenic; vaccine;
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                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                  Hanniffy
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0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apeutic; sepsis;
genital tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived
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RESULT 2
AAY49226
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                            animals, i.e. for
                                                                                polypeptides can be used for inducing an immune response in a subject which has been exposed to or infected with a pneumococcal bacterium. The can also be used for preventing infection by a pneumococcal bacterium. Vaccines comprising the polypeptides or encoding nucleic acids can be used for treating a subject infected with or exposed to a pneumococcal bacterium. Antibodies specifically binding the polypeptides can be used for detection and diagnosis and for preventing pneumococcal attachment to mucosal surface. The products can be used in humans and other animals such as domestic animals, such as feline or canine subjects, farm animals such as domestic animals, such as feline or canine subjects, farm animals
                                                        such as bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research
                                                                                                                                                                                                                  The invention provides novel isolated polypeptides comprising the amino acid sequence of an N-terminal choline binding protein A (CbpA) truncate (CbpAT). The polypeptides can be selected from sequences shown in AAY49225, AAY49227, AAY49230, AAY49231, AAY49233 and AAY49238. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choline binding protein A; CbpA; truncate; immune response; infection; pneumococcal bacterium; vaccine.
Sequence
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07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CbpA of serotype 4 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-620161/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY49226 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09951187-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 RDWGSTMKPI 322
||||||||||
369 rdwgstmkpi 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                         veterinary
                                            such as mice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462
                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0080878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
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                                                                                                                                                                                                                                                                                              9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5%;
                              medical
                                                                                                                                                                                                                                                                                             85pp; English.
                                          rats, rabbits,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                         goats,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                         sheep, pigs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                          dogs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                      animals
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Query Match 1.5
Best Local Similarity 100
Matches 10; Conservative

1.5%; sur 100.0%; Pr 100.0%; O;

Score 10; DB; Pred. No. 0.8

DB 20; 0.8;

Length 655;

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Indels

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Gaps

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RESULT :
AAY81653
ID AAY8
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AAY32099
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                                                                        Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                        This sequence represents the choline binding protein A (CbpA) of Streptococcus pneumoniae serotype type 4. The invention provides novel N-terminal CbpA truncated polypeptides (see AAV32098-110 and AAV32179-90) and polynucleotides encoding them, host-vector systems, and antibodies that specifically bind to the polypeptides. The invention also relates to vaccines including the polypeptides, which provide protection or elicit protective antibodies to bacterial infection, specifically pneumococcus, and to antibodies and antagonists against such polypeptides for use in diagnosis and passive immunotherapy. The polypeptides and/or polynucleotides are also useful as competitive inhibitors of bacterial adhesin of
AAY81653
                                                                                                                 Sequence
                                                                                                                                                                                                                                           Disclosure; Page 88-93;
                                                                                                                                                                                                                                                         New N-terminal choline binding protein A truncate polypeptides, develop products for the diagnosis, prevention and treatment of pneumococcal infections -
                                                                                                                                                                                                                                                                                                                   Tuomanen EI,
                                                                                                                                                                                                                                                                                                                                                                                                                    W09951188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    otitis media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choline binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choline binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2000
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07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                   (MEDI-)
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                                         113
                                                         616 SSSSSSDSST 625
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3 ssssssdsst 122
                                       ssssssdsst 122
                                                                                                                                                                                                                                                                                           1999-633690/54.
DB; AAZ34452.
                                                                                                                                                                                                                                                                                                                                  ST JUDE CHILDREN'S MEDIMMUNE INC.
standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding protein; CbpA; adhesin; immunogen;
diagnosis; therapy; pneumococcus; sepsis; meningitis;
                                                                                                                  655
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                   Masure
                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumonia.
                                                                                                                 ΑA;
                                                                                                                                                                                                                                                                                                                                                          98US-0056019
98US-0080878
                                                                                                                                                                                                                                                                                                                                                                                    99WO-US07669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein A (CbpA).
Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 655
                                                                                1.5%;
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                                                                                                                                                                                                                                           160pp; English
                                                                                                                                                                                                                                                                                                                   Wizemann
                                                                                                                                                                                                                                                                                                                                          RES
 694
                                                                         0;
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Pred. No.
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8
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        antibiotic;
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Best Local Similarity Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; vaccine; antibacterial; antiinflammatory; mu pneumococcal disease.
                         Antisense; prokaryotic cellular proliferation protein,
                                                                          Pseudomonas
                                                                                                                           14-FEB-2002
                                                                                                                                                                            AAU36453
                                                                                                                                                                                                                          AAU36453 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 96; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhighting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-195300/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROBIAL TECHNICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200006737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                   151 sssssdsst 160
                                                                                                                                                                                                                                                                                                                                                                                                  616 SSSSSSDSST 625
                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694
  antibacterial; drug
                                                                        aeruginosa cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l; antiinflammatory; meningitis; disease.
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hansbro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-0016337.
99US-0125164.
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                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%;
100.0%;
                                                                                                                                                                                                                               774
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No.
design
                                                                        proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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eningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
. 0.84;
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                                                                          protein #443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 694;
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RESULT
AAU35684
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klabsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                            programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                       Haemophilus influenzae cellular proliferation protein #325
                                                                                                                       AAU35684 standard; Protein; 781
                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611495/70.
N-PSDB; AAS54312.
                                                                      14-FEB-2002
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                        itp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                        67 QGGSTLTQQL 76
                                                                                                                                                                                                                                              Local Similarity 100. 
les 10; Conservative
                                                                                                                                                                                      qggstltqql 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT,
                                                                                                                                                                                                                                                                                                                774 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq ID No 12046; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                    (first entry)
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Xu HH;
                                                                                                                                                                                                                                                         1.5%;
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                                                                                                                                                                                                                                                           Score 10;
Pred. No.
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0.93;
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21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                           programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
HaSV; RNA 1; small RNA virus; replicase
                                                              12-SEP-1994
                                                                                           AAR49657;
                                                                                                                         AAR49657 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R, Yamamoto RT,
                              Sequence of Heliothis armigera replicase encoded by RNA 1.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                     ttp.wipo.int/pub/published_pct_sequences.
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Search completed: June 13, 2002, 08:46:22 Job time: 263 sec
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                                                                                                                                                                                                                                                                             The inventors claim a virus comprising a genome hybridisable with the nucleotide sequence of RNA 1 or RNA 2; pref. the sequences are those given in Figs 1 and 2 of the specification. Isolated proteins or polypeptide prepn. of the proteins or polypeptides derivable from the virus are also claimed.

H. armigera larvae were raised and viral RNA was extracted. The virus RNAs were reverse transcribed into cDNA. Clone E3 represents 99.7% or RNA 1.(hr236 contains about 88% or RNA 2.)The full length clone of RNA 1 was completed using PCR. RNA 1 encodes a protein of mol. wt. 187,000 which is regarded as the replicase in view of its AA sequence similarity in certain limited regions to replicases of of other RNA viruses. The apparent mol. wt. of this protein upon in vitro translation of virus RNA and SDS-PAGE is 195,000. The sequence given in Figure 1 is in the same sense as the viral (positive-sense) RNA. There are other small ORFs at the 3' end, corresp. to the proteins P11a, P11b and P14.
                                                                                                                                                           Query Match 1.5%; Score 10; DB 15; Length 1704; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 10; Conservative 0; Mismatches 0; Indels
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N-PSDB; AAQ58522.
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08-JUL-1993;
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Query Match

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A; Accession: G A; Status: prell A; Molecule typ A; Residues: 1- A; Cross-refere A; Experimental C; Genetics: A; Gene: Sp0369 C; Superfamily:	Science 293, 498-506, 2001 A; Authors: Loftus, B.J.; Y A; Title: Complete Genome S: A; Reference number: A95000	RESULT 1 G95042 penicillin-binding protein 1A [impo penicillin-binding protein 1A [impo C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revis C;Accession: G95042 R;Tettelin, H; Nelson, K.E.; Pauls on, J.D.; Umayam, L.A.; White, O.; nson, T.; Hickev, E.K.; Holt, I.E.		30 31 33
A;Accession: G99042 A;Status: preliminary A;Status: preliminary A;Mclecule type: DNA A;Residues: 1-719 <kur> A;Residues: 1-719 <kur> A;Residues: 1-719 <kur> A;Cross-references: GB:AE005672; PIDN:AAK74536.1; PID:g14971838; GSPDB:GN00164; TIGR:A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP0369 C;Superfamily: penicillin-binding protein 1B</kur></kur></kur>	293, 498 s: Loftu Complet	in-bindi s: Strep 03-Aug-2 ion: G95 in, H.; Umayam		10 10 10
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	nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916	RESULT 1  G95042  G95042  G95042  C;Species: Streptococcus pneumoniae  C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001  C;Accession: G95042  R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E.	ALIGNMENTS	penicillin-binding penicillin-binding penicillin-binding penicillin-binding

Qγ Ъ Qy Вb Qy B 망 DЬ Qy Ωy В Qy Qγ В δÃ Ъ Matches 666; 481 474 421 414 361 354 294 241 234 181 174 114 301 121 61 54 Local Similarity MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM 540 MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120 KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 100.0%; ilarity 100.0%; Conservative 0; Score 666; Pred. No. 0; Mismatches 0, Indels 0; Gaps 593 413 360 353 300 240 233 180 173 293 0;

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A;Title: Relatedness of penicillin-binding A;Reference number: $28031; MUID:93010977 A;Recession: $28038 A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-719 <MAR> A;Cross-references: EMBL:X67873; NID:947419 C;Superfamily: penicillin-binding protein 1
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C;Speciaes: Streptococcus pneumoniae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
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                                     KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                                                                      GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD 420
                                                                                                                                                                                         VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYNWDR
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           AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
                                                                                                                                         GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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                                                                                       KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTE
                                                                                                                                                                                                                                           TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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nces: EMBL:X67873; NID:g47419; penicillin-binding protein 1B
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99.8%;
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penicillin-binding protein 1a - Streptococcus
C;Species: Streptococcus pneumoniae
C;Date: 17-Apr-1993 *sequence_revision 17-Apr-
C;Accession: S28037
R;Martin, C; Sibold, C; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
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C;Species: Streptococcus pneumoniae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
C;Accession: S28036
A; Cross-references: C; Superfamily: penic
                              A;Status: translation not
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
                                                                                          A; Title: Relatedness of penicillin-binding A; Reference number: S28031; MUID:93010977
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C;Superfamily: penic
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A; Residues: 1-608 < MAR>
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EMBO J. 11, 3831-3836, 199
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 penicillin-binding
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 EMBL:X67872; NID:g47417; cillin-binding protein 1B
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1992
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                 PIDN:CAA48072.1;
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penicillin-binding protein 1A - Streptococcu
C:Species: Streptococcus pneumoniae
C:Date: 07-Apr-1994 #sequence_revision 07-Ap
C:Accession: A42893
R:Martin, C: Briese, T: Hakenbeck, R.
J. Bacteriol. 174, 4517-4523, 1992
A:Title: Nucleotide sequences of genes encod
A and 1B.
A:Reference number: A42893; MUID:92325042
A:Accession: A42893
A:Status: preliminary
A:Residues: 1-719 <MARN
A:Residues: 1-719 <MARN
A:Residues: 1-719 <MARN
A:Cross-references: GB:M90527; NID:9153766;
C:Superfamily: penicillin-binding protein 1B
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                                                                                                                                                                                                                                                                                              TAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYISA
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                    LOOSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMA
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                                                         NRDWGSTMKPITDYAPALEYGVYESTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
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C; Superfamily:
C; Keywords: gly
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C;Genetics:
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A97913
peptidoglycan glycosyltransferase (EC 2.4.1.129) [i C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 C;Accession: A97913
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszc R;Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Alborn Jr., W.; Arnold, Jr.; Alborn Jr., W.; Arnold, Alborn Jr.; Alborn Jr., W.; Arnold, Alborn Jr.; Alborn Jr., W.; Arnold, Alborn Jr.; Alborn Jr.;
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A; Residues: 1-719 < KI
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A; Accession: A97913
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                                                                            AAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTG
                                                                                                                                                          LQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMA
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                  RNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLT
                                                                                                                                                                                                                  NRDWGSTMKPITDYAPALEYGVYESTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
                                                                                                                                                                                                                                    NRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA 371
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                                                         AAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLSYGTG
                                                                                                                                      LQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMA
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ly: penicillin-binding protein 1B glycosyltransferase; hexosyltransferase
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..N.; Lefkowitz, E.J.;
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A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-719 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           penicillin-binding protein la - Streptococcus pneumoniae (strain 56742) (fragment) C;Speciaes: Streptococcus pneumoniae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000 C;Accession: S28034 R;Martin, C.; Sibold, C.; Hakenbeck, R. EMBO J. 11, 3831-3836, 1992
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Matches 181
                                                                                                                                                                                             Query Match 27.2%; S
Best Local Similarity 100.0%;
Matches 181; Conservative 0;
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                                                              IRILGAFLRNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATK 110
QETLTYYINKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPE
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                                                                                                                                                                                                 Score 181; DB 2; L
Pred. No. 5.5e-175;
0; Mismatches 0;
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                               Query Match
Best Local Similarity
Matches 181; Conserv
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penicillin-binding protein la - Streptococcus pneumoniae (strain 681) (fragment) (Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000 C;Accession: S28032 R;Martin, C.; Sibold, C.; Hakenbeck, R. EMBO J. 11, 3831-3836, 1992 EMBO J. 11, 3831-3836, 1992 A;Title: Relatedness of penicillin-binding protein la genes from different clone: A;Reference number: S28031; MUID:93010977
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C;Species: Streptococcus pneumoniae
C;Date: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 26-May-2000
C;Accession: S28033
C;Accession: S28033
R;Martin, C; Sibold, C; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
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S28032
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A;Cross-references: EMBL:X67866; NID:g47407; C;Superfamily: penicillin-binding protein 1B
                               A;Accession: S28032
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
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A; Residues: 1-719 <MAR>
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Pred. No. 5.5e-175;
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                 PIDN:CAA48066.1; PID:g47408
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Score 181; I Pred. No. 5.

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A; Reference number: S28031; MUID:93010977
A; Accession: S28035
A; Stature
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S28035
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R;Martin, C.; Sibold, C.; Hakenbeck,
EMBO J. 11, 3831-3836, 1992
A;Title: Relatedness of penicillin-b.
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C;Superfamily: penicillin-binding protein 1B
C;Keywords: antibiotic resistance; penicillin
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A; Residues: 1-188 <KEL>
A; Cross-references: EMBL: Z21800
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A;Variety: strain 85983
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C;Accession: S31952
R;Kell, C.M.; Jordens, Z.; Daniels, M.; Coffey, T.J.; Bates, J.; Paul, J.; Gilks, R;Kell, C.M.; Jordens, Z.; Daniels, M.;
                                                                                          A; Experimental source: strain 2039 C; Superfamily: penicillin-binding
                                                                                                        A;Cross-references: EMBL:X67870; NID:g47413; PIDN:CAA48070.1; A;Experimental source: strain 2039
                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-719 <MAR>
                                                                                                                                                                                                                                                                                               A; Variety: strain 2039
C; Date: 17-Apr-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                   penicillin-binding protein IA - Streptococcus C;Species: Streptococcus pnawmoni-
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, February 1993
A;Description: Molecular epidemiology of penicillin-resistant pneumococci isolated in A;Reference number: S31941
A;Accession: S31952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                            C; Keywords:
                                                                                                                                                                             A; Status: translation not shown
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          Query Match
Best Local
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Best Local
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                                                                            antibiotic
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97; Conser
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       Similarity
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                                                                          resistance;
       11.9%;
100.0%;
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Pred. No.
       Score
Pred.
                                                                                          protein 1B
                                                                          penicillin
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 79;
No.
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       DB 2; L; 2.2e-71;
                                                                          resistance
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                       Length 719
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                                                                                                                          PID:g47414
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                                                                                                                                                                                                                                                                                                                                                 2039) (fragment)
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penicillin-binding protein 1A [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                     RESULT
G86692
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A; ACCESSION.
A; Molecule type: DNA
A; Residues: 1-139 < KEL>
A; Cross-references: EMB1: Z21809; NID: 949384; P:
A; Experimental source: strain 100511
C; Superfamily: penicillin-binding protein 1B
C; Superfamily: antibiotic resistance; penicillin
                                                                                                                                                                                                                                                                      R;Kell, C.M.; Jordens, Z.; Daniels, M.; Coffey, T.J.; Bates, J.; Paul, J.; Gilks, esubmitted to the EMBL Data Library, February 1993
A;Description: Molecular epidemiology of penicillin-resistant pneumococci isolated A;Reference number: S31941
                                                                                                                                                                                                                                                                                                                                                      C:Species: Streptococcus pneumoniae
A;Variety: strain 100511
C:Date: 06-Jan-1995 #sequence_revision
                                                                                                                                                                                                                                                         A; Reference number: A; Accession: S31941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M90528; NID:g153769
C;Superfamily: penicillin-binding protein
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A; Residues: 1-637 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Martin, C.; Briese, T.; Hakenbeck, J. Bacteriol. 174, 4517-4523, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          penicillin-binding protein 1 - Streptococcus oralis
C;Species: Streptococcus oralis
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
                                                                                                                                                                                                                                                                                                                                       C; Accession: S31941
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16
                                                                                 Local
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GYTRKYSMAVWTGYSNRLTP
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llarity 100.0%;
Conservative 0;
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A42893;
                                                                                                                                                                                                                                                                                                                                                                                                           1A - Streptococcus pneumoniae (strain 100511) (fragment)
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Pred. No.
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                                                                                 DB 2; I
4.1e-12;
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                                                                                                                                                                                                     PIDN:CAA79874.1;
                                                                                                                                                     resistance
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penicillin-binding protein 1B [imported] - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A; Experimental source: C; Genetics: A; Gene: pbp1B
                                                             A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Recession: B86673 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-801 <STO>
                                                                                                                                                                                 C; Accession: B86673
R; Bolotin, A.; Wincker, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain C; Genetics: A; Gene: mrcB; BU200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-760 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome sequence of A;Reference number: A84930; A;Accession: E84953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
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E84953
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-664 <STO>
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: G86692
R; Bolotin, A.; Wincker, P.;
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C; Superfamily:
                                                                                                                                                                                                                                                                       B86673
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                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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Best Local
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12; Conserv
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                                 GB:AE005176; PID:g12723258; PIDN:AAK04484.1; GSPDB:GN00146
ce: strain IL1403
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0.0025;
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C; Genetics:
A; Gene: pbp1
C; Keywords:
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A; Authors. Toffin.
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                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-821 <KUR>
                                                                                                                                                                                                                                                      A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C. A; Title: Genome of the Bacterium Streptococcus pneumoniae A; Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                          peptidoglycan glycosyltransferase (EC 2.4.1.129) [imported] - Streptococcus
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
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C;Date: 03-Aug-2001 #sequence_revision
C;Accession: E95245
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A; Residues: 1-821 < KUR>
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Authors: Yang, Y. vo....
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                                                   Query Match
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Strain R6
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hypothetical protein F53G12.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T29028 R;Mu, X.; Graves, T.
                                                                               hypothetical protein F25H9.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T21377 R;Smye, R.
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A;Molecule type: DNA
A;Mesidues: 1-966 <STO>
A;Cross-references: GB:AP001518; GB:BA0000004; NID:g10175792;
A;Cross-references: GB:AP001518; CB:BA0000004; NID:g10175792;
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A; Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Sterens. E84053
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             A;Reference number: Z19414
A;Accession: T21377
A;Status: preliminary; translated f
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A; Introns: 111/3;
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A;Experimental source: strain Bristol N2; clone F53G12
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A; Residues: 1-294 <WUX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, May 1997 A; Description: The sequence of C. elegans cosmid F53G12
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A;Gene: pdp
A; Molecule
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.K.; Kadune, D.; Holley, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916
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                                                                                                                                                           C;Date: 03-Aug-2001 #sequence_revision
C;Accession: H95255
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H95255
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A;Residues: 1-106,'A',108-577 <SCH2>
A;Cross-references: GB:J05484; NID:g168840; PIDN:AAA33597.1; PID:g168841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Neurospora crassa
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C;Accession: A36442; S35362
R;Schneider, H.; Arretz, M.; Wachter, E.; Neupert, W.
J. Biol. Chem. 265, 9881-9887, 1990
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A:Introns: 7/1; 34/3; 88/1; 189/3; 277/2; 343/3; 442/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F25H9
A; Reference number: A; Accession: H95255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-577 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondrial processing peptidase (EC 3.4.24.64) alpha chain precursor - N,Alternate names: alpha-MPP; mitochondrial processing peptidase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP: F25H9.5
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-504 <WIL>
A; Cross-references: EMB
                                                                                                                                              R; Tettelin, H.; Nelson,
                                                                                                                                                                                                                             choline binding protein A [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Genome:
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llarity 100.0%;
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                                                                                                                        K.E.; Paulsen, I.T.; Eisen, J.A.; White, O.; Salzberg, S.L.; Lewis,
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No.
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                                                                                                                                                                                                                                Streptococcus pneumoniae
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.19;
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M.R.;
                                                                                                                          T.D.; Peterson, S.; H
Radune, D.; Holtzappl
                                                                                                                                                                                        03-Aug-2001
                                                                                                                                                                                                                                (strain TIGR4)
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A; Gene: I
A; Map po
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
A;Accession: AI3480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005672; PIDN:AAK76241.1; PID:g14973701; GSPDB:GN00164; TIGR:SP-A;Experimental source: strain TIGR4
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A;Molecule type: DNA
A;Residues: 1-693 <KUR>
                                                                                                                                       A; Cross-references: GB:AE007869;
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-757 < KUR>
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A; Accession: G97472
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C;Species: Agrobacterium tumefaciens
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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C; Species: Brucella melitensis
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A;Gene: SP2190
                                                                                    A;Gene: AGR_C_1696
A;Map position: ci
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score 10; DB; Pred. No. 0.2 0; Mismatches
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                 DB 2;
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                 RESULT
AB2589
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A;Reference number: A97359; PMID:11743194
A;Accession: B97371
A;Status.
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A; Molecule type: DNA
A; Residues: 1-757 <KUR>
A; Cross-references: GB: AEO08688; PIDN: AAL41945.1;
A; Cross-references: Strain C58 (Dupont)
                            Qy
                                                                                                                                                                                                                                                                       R:Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pa
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A; Gene: Atu0931
A; Map position:
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A;Map position: circular
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C;Genetics:
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A; Residues: 1-764 < KUR>
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C; Species: Agrobacterium tumefaciens
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change
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294, 2317-2323, 2001
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QGGSTLTQQL 192
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                                                                          Similarity
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                                                             Conservative
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                                                                                                                                                                                   GB:AE007869; PIDN:AAK85923.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
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                                                                                                                                        chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%;
                                                                          1.5%;
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                                                                            .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                          Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10;
Pred. No.
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.; Jung, M.; Krespan, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                       Miller, N.; Doughty, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
0.27;
                                                                          0.2
                                                                          B 2;
                                                                                                                                                                                                                                                                          and Biotechnology Agent Agrobacterium
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                                                                                                                                                                                   PID:g15154974; GSPDB:GN00169
                                                             0;
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                                                                                                                                                                                                                                                                                                       Blanchard, M.; Qurollo, Scott, C.; Lappas, C.;
                                                                                       Length 764
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                                                                                                                                                                                                                                                                                                                                                                                   tumefaciens (strain
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                                                                                                                                                                                                                                                                                                                                                      11-Jan-2002
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                        B.; Gold
Markelz,
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protein pbpC [imported] -

Agrobacterium

tumefaciens (strain

C58,

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C; Species: Agrobacte
C; Date: 11-Jan-2002
C; Accession: AB2589
R; Wood, D.W.; Setuba
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho
                                                                                                                                               penicillin-binding protein 1B VC0602 [imported] - Vibrio cholerae (strain N
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A82303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         penicillin-binding protein 1B PA4700 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-3000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83057 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Coulter, S.N.; Folger, R.; Coulter, S.N.; Folger, K.R.; Coulter, S.N.; Folger, R.; Coulter, S.N.; Folger, 
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go
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A; Residues: 1-774 <STO>
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A; Residues: 1-764 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004884; GB:AE004091; NID:g9950954; PIDN:AAG08086.1; GSPDB:GN00
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                             220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 QGGSTLTQQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          QGGSTLTQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGSTLTQQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enome sequence of Pseudomonas
A82950; MUID:20437337
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Pred. No.
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0.27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
pathogen Vibrio cholerae
                                                                                                                                                                                                                                          cholerae (strain N16961
                                                                                       Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perry, M.; Gordon-Kamm
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                                                                                                                   R.J
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                         A;Gene: mrcI
C;Keywords:
                                                                                                                                                                                                                                    A;Title: Genome sequence of A;Reference number: AB0001; A;Accession: AC0412
                                                                                                                                                                                                                                                                                                                        deno-Tarraga, A.M.; Chillingworth, T.;
il, M.; Rutherford, K.; Simmonds, M.;
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001 C;Accession: AC0412 (C;Accession: AC0412 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
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                                                                                       C; Genetics:
                                                                                                                A; Molecule type: DNA
A; Residues: 1-824 <KUR>
A; Cross-references: GB:
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C; Superfamily: penicillin-binding
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A; Residues: 1-777 <HEI>
                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          penicillin-binding protein 1B
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                            pentosyltransferase
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; Cronin, A.; Davies, R.M.; Skelton, J.; Stevens, K.; V

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R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Frine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630
A;Accession: D64138
                                                                                                           A;Molecule type: DNA
A;Residues: 1-781 <TIGR>
A;Cross-references: GB:U32845; GB:L42023;
C;Superfamily: penicillin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
C;Accession: D64138
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A;Accession: A82303
A;Status: preliminary
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Qy 67 QGGSTLTQQL 76

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Search completed: June 13, 2002, 08:49:14

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MEDLINE=93010977; PubMed=1396576;
Martin C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein la genes from clones of penicillin-resistant Streptococcus pneumoniae i South Africa and Spain.";
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95020625; PubMed=7934910; Pearce B.J., Yin Y.B., Masure H.R.
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Science 293:498-506(2001).
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MISCELLANEOUS: THESE STRAINS ARE PENICILLIN-SENSITIVE.
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PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN
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Q00573;
Q1-OCT-1994
Q1-OCT-1994
15-DEC-1998
MEDIINE=92325042; PubMed=1624444;
Martin C., Briese T., Hakenbeck R.;
"Nucleotide sequences of genes encoding penicillin-binding from Streptcocccus pneumoniae and Streptcocccus oralis with homology to Escherichia coli penicillin-binding proteins la J. Bacteriol. 174:4517-4523(1992).
                                                                                                                                                                                                                                                         _STROR
                                                                SEQUENCE FROM N.A. MEDLINE=92325042; Publ Martin C., Briese T.,
                                                                                                                Streptococcus.
NCBI_TaxID=1303;
                                                                                                                                          Bacteria; Firmicutes;
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(Rel. 30, Last sequence update)
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binding protein 1A (PBP-1A) (Fra
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                                                                                                                                         Bacillus/Clostridium group; Streptococcaceae;
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STRAIN-TOKYO 1998;

STAIN-TOKYO 1998;

MEDLINE-20445173; PubMed-10993077;

MEDLINE-20445173; PubMed-10993077;

MEDLINE-20445173; PubMed-10993077;

MEDLINE-20465173; PubMed-10993077;

MEDLINE-20465173; PubMed-10993077;

MEDLINE-20465173; PubMed-10993077;

MEDLINE-20465173; PubMed-10993077;

MEDLINE-20465174; PubMed-10993077;

MEDLINE-204651745; PubMed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidoglycan synthesis; An Multifunctional enzyme. Multifunctional enzyme. AcT_SITE 371 371 NON_TER 637 637 AA; 70891 M
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P57296;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1B (PBP-1b) (PBPIb) (Murein pol)
[Includes: Penicillin-insensitive transglycosylase (EC 2.4.
(Peptidoglycan TGase); Penicillin-sensitive transpeptidase
(EC 3.4.--) (DD-transpeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Antibiotic resistance; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      symbiotic bacterium).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M90528; AAA26958.1; -.
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                                                                                  TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL
TRANSPEPTIDASE FAMILY.
                                                                                                                                                      PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SIMILARITY: IN THE N-TERMINAL SECTION;
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53; Conservative
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SEQUENCE 90277682; PubMed=2141023;
Schneider H., Arretz M., Wachter
Schneider Geptidase of m
                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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or send a
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precursor proteins imported into the mitochondrion, typica
Arg in position P2.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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01-MAR-1992 (Rel.
16-OCT-2001 (Rel.
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Interpro; IP001264; Transglycosyl.
Pfam; PF00912; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrial processing precursor (EC 3.4.24.64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00912; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
Hydrolase; Multifunctional enzyme; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                   relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                    Sordariales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPPA_NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                  SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
SUBCELLULAR LOCATION: Mitochondrial matrix.
DOMAIN: APPEARS TO CONTAIN TWO DOMAINS OF APPROXIMATELY EQUAL
WHICH ARE SEPARATED BY A LOOP-LIKE SEQUENCE.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16; ALSO KNOWN AS THE
INSULINASE FAMILY. DOES NOT SEEM TO HAVE A PROTEASE ACTIVITY.
                                                                                                                                                                                                                                                           Biol. Chem. 265:9881-9887(1990).
FUNCTION: THE MITOCHONDRIAL PROCESSING PROTEASE CLIPPESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGGSTLTQQLIK 78
J05484; AAA33597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (S an email to license@isb-sib.ch).
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136
392
451
760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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308
684
451
88002
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40, Last annotation update)
cessing peptidase alpha subunit, mitochondrial
.24.64) (Alpha-MPP).
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CYTOPLASMIC
 ALT_SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL) TRANSGLYCOSYLASE. TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYLATED BY PENICILLIN (BY SIMILARITY) 00B2C5B51F6947D3 CRC64;
                                                                                                                                                                                                                                                                                                                 r E., Neupert W.;
mitochondria. Structure-function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577
                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
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                                                                                                                                                                                                                                                                                                                                                                                                                Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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Best Local
                                                                between
the Euro
                                                                                                                                                                                                                                                                                                                                                                         Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettein H., Richardson D., Ermolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1B (PBP-1b) (PBP1b) (Murein polymerase)
[Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-)
(Peptidoglycan TGase); Penicillin-sensitive transpeptidase
(EC 3.4...) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20406833; PubMed=10952301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PBPB_VIBCH Q9KUC0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P31800; 1BE3.
InterPro; IPR00143; Peptidase_M16.
Pfam; PF00675; Peptidase_M16; 1.
PROSITE; PS00143; INSULINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A36442; A36442.
HSSP; P31800; 1BE3.
                                                                                                                                                                                                                                                                                                                                      cnoterae
                                                                                                                                                                                                                                                                                                                                                   "DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRCB OR PONB OR VC0602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Metalloprotease; Mitochondrion; Transit peptide TRANSIT 1 35 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ESSSSSSSS 295
                                                                                                                        TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION;
TRANSPEPTIDASE FAMILY.
                                                                                                                                                  Similarity).
SIMILARITY: IN THE N-TERMINAL
TRANSGLYCOSYLASE FAMILY.
                                                                                                                                                                            SUBCELLULAR LOCATION: Type II membrance similarity).
                                                                                                                                                                                                               FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEDFIDGLYCAN FROM THE LIPID INTERREDIATES. THE ENZYME HAS A PENICILLIN-INSENSITIVE TRANSCLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPETIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY STALLARITY) DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY STALLARITY) TO SUBUNITS OF THE PEPTIDE SUBUNITS OF THAL STAGES IN PEPTIDGLYCAN SYNTHESIS.
                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESSSSSSDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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577 p
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                                                                                                                                                                                                                                                                                                                                                 of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER-RICH
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0.081;
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                                                                                                                                                                                                   protein.
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use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).

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http://www.isb-sib.ch/announce/

EMBL; AE004145; AAF93769.1; TIGR; VC0602; -

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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-RD / KW20 / ATCC 51907;

MEDLIND-95350630; PubMed-7542800;

REDLIND-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidhan J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1B (PBP-1b) (PBP1b) (Murein polymerase)
[Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-)
[Peptidoglycan TGase); Penicillin-sensitive transpeptidase
[EC 3.4.--) (DD-transpeptidase)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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ACT_SITE
SEQUENCE
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P45345;
                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
Science 269:496-512(1995),
-i-FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKE
           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 3.4.-.-) (DD-transpeptidase)].
MRCB OR PONB OR HI1725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIRM: PFU0912; TRANSGLYCOSY1; 1.

ProDom; PD001895; Transglycosy1; 1.

Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Hydrolase; Antibiotic resistance; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                            FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PREFIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A PRINCILLIN-INSENSTITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPECTIDASE C.TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
                                                                                                                                          SUBUNITS) (BY SIMILARITY).

PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

SUBCELLULAR LOCATION: Inner membrane (By similarit

SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO
                                                                                    TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                              TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGGSTLTQQL 239
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pfam; pF00912; Transplycosyl; 1.

pfam; pF00905; Transpeptidase; 1.

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proDom; pD001895; Transplycosyl; 1.

protioglycan synthesis; Cell wall; Transferase; Glycosyltransferase;

medical communication of the comm
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use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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L. J. Med. Microbiol. 50:828-832(2001).

R. EMBL; AR210745; AAF17255.1; -.

R. InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transpeptdse.

Pfam; PF00912; Transglycosyl; 1.

Pfam; PF00905; Transglycosyl; 1.

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SEQUENCE 719 AA; 79758 MW; 5BD397E83B4B3AA6 CRC64:
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NCBI_TaxID=1313;
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serotype 23F from the nasopharyngeal flora of
J. Med. Microbiol. 50:828-83 (2001).
EMBL; AF210746; AAF17256.1;
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
pfam; PF00912; Transglycosyl; 1.
pfam; PF00912; Transpeptldase; 1.
PFODOm; PF0001895; Transglycosyl; 1.
PFODOm; PF001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79830 MW; 5F6776B8DEAE38
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Streptococcus
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MEDLINE=21432820; PubMed=11549185;
Ferroni A., Berche P.;
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NCBI_TaxID=1313;
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SEQUENCE
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Q9RET3; O1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-DEC-2001 (TrEMBLrel. 19,
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InterPro: IPR001460; Transpeptdse.
Pfam; PF009012; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
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Marthn C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein la genes from different
clones of penicillin-resistant Streptococcus pneumoniae isolated ir
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NCBI_TaxID=1313;
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EMBO J. 11:3831-3836(1992).
EMBL; X67871; CAA48071.1; -
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Bacteria; Firmicutes; Bacillus/Clostridium
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SEQUENCE FROm ...

STRAIN=#10/Z19;

X MEDLINE=98409715; PubMed=9736547;

A Asahi Y. Ubukata K.;

"Association of a Thr-371 substitution in RT of penicillin-binding protein 1A with pennicillin-binding protein 1A
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O9R7M6;
O1-MAY-2000 (TrEMBLrel. 13, Cr
f 01-MAY-2000 (TrEMBLrel. 13, Lr
T 01-DEC-2001 (TREMBLREL. 19, L
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J. Med. Microbiol. 50:828-832(2001).

EMBL; AF210752; AAF17262.1; -.

R EMBL; AF210752; AAF17262.1; -.

R InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transpeptdse.

R Pfam; PF009012; Transglycosyl. 1.

R Pfam; PF009015; Transglycosyl; 1.

R ProDom; PD001895; Transglycosyl; 1.

R ProDom; PD001895; Transglycosyl; 1.

SEQUENCE 719 AA; 79781 MW; DB5993F6BD47F72D CRC64;
                                                                                                                                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
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"Genetic analysis of clinical isolate "Genetic analysis of clinical isolate with high-level resistance to expande Antimicrob. Agents Chemother. 39:1306 EMBL; Z49095; CAA88918-1; ...

EMBL; Z49095; CAA88917-1; ...

InterPro; IPRO01264; Transglycosyl. InterPro; IPRO01264; Transglycosyl. InterPro; IPRO01460; Transpeptidse. Pfam; PF009012; Transglycosyl; 1. Probom; PD001895; Transglycosyl; 1. Probom; PD001895; Transglycosyl; 1. SEQUENCE 719 AA; 79712 MW; 539661
                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS111 (CEPHALOSPORIN-RESISTANT CLINICAL
STRAINE=96012191; PubMed=7574521;
MEDLINE=96012191; PubMed=7574521;
Coffev T.J., Daniels M., McDougal L.K., Dowson
                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLIEL 01, 01-NOV-1996 (TREMBLIEL 01, 01-JUN-2001 (TREMBLIEL 17, PENICILLIN-BINDING PROTEIN
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InterPro; IPR001460; Transpeptdse.
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39:1306-1313(1995).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                             MEDLINE-98287565; PubMed=9624469;
Smith A.M., Klugman K.P.;
"Alterations in PBP IA essential for
                                                                                                                                                                                                                                                  in Streptococcus pneumoniae.";
Antimicrob. Agents Chemother. 42:1329-1333(1998).
EMBL; AF046233; AAC24698.1; -.
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"Alterations in PBP IA essential for high-level penicillin
in Streptococcus pneumoniae.";
Antimicrob. Agents Chemother. 42:1329-1333(1998).
EMBL; AF046235; AAC24700.1;
InterPro; IPR001460; Transpeptdse.
Pfam; PF00905; Transpeptidase; 1.
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Smith A.M., Klugman K.P.;
"Alterations in PBP 1A essential for high-level penicillin
in Streptococcus pneumoniae.";
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Best Loc
Matches
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Best Local Similarity 100.0%;
Matches 223; Conservative
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STRAIN=17619;
MEDLINE=98287565; PubMed=9624469;
Smith A.M., Klugman K.P.;
Smith A.M., Klugman K.P.;
"Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-level penicillin resistance "Alterations in PBP 1A essential for high-
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01-JUN-1998 (TrEMBLrel.
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Db Qy

437 181

FANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT

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FANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT

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Best Local Similarity 100.0%;
Matches 207; Conservative
STRAIN=SP 1258;
MEDLINE=21432820;
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01-mAY-2000 (TrEMBLrel. 13,
01-mAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
PENICILLIN-BINDING PROTEIN)
                                                                                                               Streptococcus.
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Smith A.M., Klugman K.P.;
"Alterations in PBP 1A essential for high-level penicillin resistance
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01-JUN-1998 (TrembLrel. 06,
01-JUN-1998 (TrembLrel. 06,
01-DEC-2001 (TrembLrel. 19,
PENICILLIN-BINDING PROTEIN
                                          SEQUENCE FROM N.A.
                                                                                                                                     Bacteria; Firmicutes;
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Antimicrob. Agents Chemother. 42:1329-1333(1998).
EMBL; AF046234; AAC24699.1;
InterPro; IPR001460; Transpeptdse.
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Best Local Similarity
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"Alterations to penicillin-binding proteins 1A, 2B and 2x amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23f from the nasopharyngeal flora of children.";

J. Med. Microbiol. 50:828-832(2001).

EMBL; AF210748; AAF17258.1;

EMBL; AF210748; AAF17258.1;

InterPro; IPR001264; Transglycosyl.

InterPro; IPR001460; Transpeptdse.
Pfam; PF00905; Transpeptidse: 1.

Pfam; PF00905; Transpeptidse: 1.

ProDom; PD001895; Transglycosyl; 1.

ProDom; PD001895; Transglycosyl; 1.
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"Association of a Thr-371 substitution
of penicillin-binding protein 1A with
                                                                                                                                                                                                                                  STRAIN=#1/H23;
MEDLINE=98409715; PubMed=9736547;
                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1313;
[1]
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01-DEC-2001
                                                                                                                                                   Antimicrob. Agents Chemother. 42:2267-2273(1998).
EMBL; AB006868; BAA32064.1; -
InterPro; IPR001460; Transpeptuse.
                                                                                                                                                                                                                                                                                                              Streptococcus pneumoni Bacteria; Firmicutes;
                                                                                                                                           Pfam;
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79715 MW;
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(Coffey T.J., Daniels M., Enright M.C., Spratt B.G.;

(T "Serotype 14 variants of the Spanish penicillin-resistant serotype 9v

(T clone of Streptococcus pneumoniae arose by large recombinational

(T replacements of the cpsA-pbpla region.";

(L Microbiology 145:0-0(1999).

(R EMBL; AF13989); AADA3073.1; -.

(R EMBL; AF13988); AADA3070.1; -.

(R EMBL; AF13988); AADA3071.1; -.

(R EMBL; AF13988); AADA3072.1; -.

(R EMBL; AF13988); AADA48072.1; -.

(R EMBL; AF13988); AADA48430.1; -.

(R EMBL; AF139448); AADA48430.1; -.

(R EMBL; AF159448); AADA48430.1; -.

(R EMBL; AF13988);                                                                                                                                                                                                                                                                                       Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=URU-E159, M134,
Coffey T.J., Daniels N
"Serotype 14 variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumon Bacteria; Firmicutes;
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                                                       AAQDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQV
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                                     AAQDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQV
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so 14 variants of the Spanish penicillin-resistant serotype
Streptococcus pneumoniae arose by large recombinational
lents of the cpsA-pbpla region.";
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100.0%;
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Q54946;
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1996 (TIEMBLIEL 0
01-CCT-2001 (TIEMBLIEL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein 1a clones of penicillin-resistant Streptococcus South Africa and Spain.";
EMBO J. 11:3831-3836(1992).
                                                                                                                                                                                                                   clone of Streptococcus pneumoni
replacements of the cpsA-pbpla
Microbiology 0:0-0(199)
EMBL; X67868; CAA48068 1; -.
                                                                                                                                                                                                                                             Coffey T.J., Daniels M., Enright M.C., Spratt B.G.; "Serotype 14 variants of the Spanish penicillin-resistant serotype clone of Streptococcus pneumoniae arose by large recombinational
                                                                                                                                                                                                                                                                                                                          "Association of a thr-371 substitution of penicillin-binding protein 1A with I
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 320-717 FROM N.A.
STRAIN=#17/Z46, #20/B98, AND #27/SHA3;
MEDLINE=98409715; PubMed=9736547;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 310-619 FROM STRAIN=8303, AND 35193; Smith A.M., Klugman K.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93010977;
Martin C., Sibold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                             STRAIN-SP-665
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QEILTYYINKVYMSNGNYGMOTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPE 170
                                     [T]
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C., Hakenbeck R.;
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Best Local S
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EMBL; AP139886; AAD43069.1; -

EMBL; AF139884; AAD43067.1; -

EMBL; AF139885; AAD43068.1; -

EMBL; AF139885; AAD43068.1; -

InterPro; IPR001264; Transglycosyl.

InterPro: IPR001460; Transpeptidse.

Pfam; PF00912; Transglycosyl; 1.

Pfam; PF00905; Transglycosyl; 1.

ProDom; PD001895; Transglycosyl; 1.

SEQUENCE 719 AA; 79622 MW; 7FBA6A
                                 O9RET6;
01-mAY-2000 (TrEMBLrel. 13,
01-mAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
PENICILLIN-BINDING PROTEIN 1
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
PENICILLIN-BINDING PROTEIN 1A.
                                                                                         Q9RET6
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Coffey T.J., Daniels M., Enright M.C., Spratt B.G.;
"Serotype 1.4 variants of the Spanish penicillin-resistant serotype
clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PO-342, PO-27;
Coffey T.J., Daniels
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 Bacteria;
            Streptococcus
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Bacillus/Clostridium group; Streptococcaceae;
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                                              Last annotation
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Best Local Sin
Matches 181;
penicillin-resistant clinical isolates of Streptococcus serotype 23F from the nasopharyngeal flora of children.
J. Med. Microbiol. 50:828-832(2001).
EMBL; AF210751; AAF17261.1;
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transpeptidase.
Pfam; PF00912; Transpeptidase; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79567 MW; 7B6EDCCBB8BCF286 CRC64;
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O1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-DEC-2001 (TrEMBLrel. 19,
PENICILLIN-BINDING PROTEIN
                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-SP 22861;
MEDLINE-21432820; PubMed-11549185;
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EMBL; AF210749; AAF17259.1; ...
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79638 MW; 1DAE3C5937048E16 CRC64;
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Ferroni A., Berche P.;
"Alterations to penicillin-binding proteins 1A, 2B and 2X amongst
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NCBI_TaxID=1313;
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Query Match

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InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptdase; 1.
ProDom; PD001895; Transglycosyl; 1.
NON_TER 719 719
SEQUENCE 719 AA; 79710 MW; D90EB4
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Q54947;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
                                                                                                                                                                                                                                                                                                   South Africa and Spain.";
EMBO J. 11:3831-3836(1992).
EMBL; X67866; CAA48066.1; -
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Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transgeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
NON_TER 719 719
SEQUENCE 719 AA; 79611 MW; 1DBFDI
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Q54949;
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Q1-NOV-1996
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Q54948;
01-NOV-1996
SEQUENCE FROM N.A.
STRAIN=56742;
MEDLINE=93010977; PubMed=1396576;
MARTLI C., Sibold C., Hakenbeck R.;
"Relatedness of penicillin-binding protein la genes clones of penicillin-resistant Streptococcus pneumon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin C., Sibold C., Hakenbeck R.; Relatedness of penicillin-binding protein la clones of penicillin-resistant Streptococcus psouth Africa and Spain.";
                                                                 Streptococcus.
NCBI_TaxID=1313;
                                                                                      Streptococcus
Bacteria; Fire
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01-JUN-2001
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EMBL; X67867; CAA48067.1; -
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-BINDING PROTEIN 1
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SEQUENCE
                                                                                                                                                                                        Overweg K., Bogaert D., Sluijter M., de Groot R., Herman "Molecular characterization of Streptococcus pneumoniae resistance in the Netherlands.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ403978; CAC20960.1; -.
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
Pfam; PF00905; Transglycosyl; 1.
Pf0Dom; PD001895; Transglycosyl; 1.
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J. 11:3831-3836(1992).
                                ELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYG
                                                            SNYPAYMDNYLKEVINQVEEETGYNLLTTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDD
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Best Local Similarity
Matches 142; Conser
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01-MAR-2001
01-MAR-2001
Overweg K., Bogaert D., Sluijter M., de Groot "Molecular characterization of Streptococcus resistance in the Netherlands." Submitted (MAY-2000) to the EMBL/GenBank/DDB: EMBL; AJ403977; CAC20959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    Q9EW43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     penicillin-resistant clinical isolates of S serotype 23F from the nasopharyngeal flora J. Med. Microbiol. 50:828-832(2001).
EMBL; AF210747; AAR17257.1;
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
                                                                                                                                                               Streptococcus.
NCBI_TaxID=1313;
[1]
                                                                                                                                                                                                                           Streptococcus pneumon:
Bacteria; Firmicutes;
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Pfam; PF00905; Transpeptidase; 1.
Probom; PD001895; Transpelycosyl;
SEQUENCE 719 AA; 79662 MW; A7
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                 STRAIN-950421;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              PENICILLIN
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3Lrel. 16, Last anno
3 PROTEIN 1A (FRAGME
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                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local Similarity
Matches 139; Conserv
Q9RET5;
Q9RET5;
01-MAY-2000
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01-JUN-1998 (TrEMBLrel. 06, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotation profile)
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                 Smith A.M., Klugman K.P.;
"Alterations in PBP lA essential for high-level penicillin resistance in Streptococcus pneumoniae.";
Antimicrob. Agents Chemother. 42:1329-1333(1998).
EMBL., AF046332; AAC24697.1; ...
EMBL., AF046332; AAC24697.1; ...
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                                                                                                     SSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKE
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nicutes; Bacillus/Clostridium
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Best Local Similarity
Matches 105; Conserv
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Best Local
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
PENICILLIN BINDING PROTEIN 1
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-#2/H26 #4/H29, #13/Z34, #18/B43,
MEDLINE-98409715; PubMed-9736547;
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                                                                                                      SEQUENCE
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NCBI_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EILTYYINKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEA
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15.8%; Score 105; Itarity 100.0%; Pred. No. 5. Conservative 0; Mismatches
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43610 MW;
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Last annotation update)
LA (FRAGMENT).
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Pred. No.
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                                                                                                      1A29B32C7630D56A CRC64;
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Best Local S
Matches 105
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PENICILLIN B
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"Association of a Thr-371 substitution in a conse;
of penicillin-binding protein 1A with penicillin
Streptococcus pneumoniae.";
Antimicrob. Agents Chemother. 42:2267-2273(1998).
EMBL; AB006872; BAA33068.1;
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087105;
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NON_TER
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STRAIN=#7/KK133;
MEDLINE=98409715; PubMed=9736547;
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Bacteria; Firmicutes; Bacillus/Clostridium
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of penicillin-binding protein Streptococcus pneumoniae.";
                        Asahi Y., Ubukata K.;
"Association of a Thr-371 substitution in
of penicillin-binding protein 1A with per
                                                                                                   MEDLINE=98409715; PubMed=9736547;
                                                                                                                                  SEQUENCE FROM N.A. STRAIN=#9/Z17;
                                                                                                                                                                                                                                           Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                 98 (TrEMBLrel. 08, 098 (TrEMBLrel. 08, 101) (TrEMBLrel. 19, 101) N BINDING PROTEIN 1.
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(TremBLrel. 13, Last sequence update)
(TremBLrel. 17, Last annotation update)
BINDING PROTEIN 1A (FRAGMENT).
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la (FRAGMENT).
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Pred. No. 5.3e-98;
0; Mismatches 0;
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01-JUN-1998 (TrEMBL)
01-JUN-1998 (TrEMBL)
01-DEC-2001 (TrEMBL)
PENICILLIN-BINDING I
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Q54918;
Q1-NOV-1996
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                                                                                                                                                                                                                                                                                                    Streptococcus pneumoni
Bacteria; Firmicutes;
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                                                                                                                                         SEQUENCE
                                                                                                                                                                          EMBL;
                                                                                                                                                                                   Infect.
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                                                                                                                                                                                                                                                                                                                                     (FRAGMENT).
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152
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                                          92
                                                                                                                                                                                Nairobi, Kenya.";
fect Immun 61:4382-4391(1993).
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                                         SSDSSTSQSSSTTPSTNNSTTINPNNNTQQSNTTPDQQNQNPQPA
SSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTP
          SSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTP 654
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100.0%;
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. 01, Last sequence update)
. 19, Last annotation update)
PENICILLIN-BINDING PROTEIN 1A GENE
                                                                                                                                          MW;
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Pred. No. 5.
                                                                                                Score 98;
Pred. No.
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"Association of a Thr-371 substitution in a conserved amino acid motif of penicillin-binding protein IA with penicillin resistance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumon:
Bacteria; Firmicutes;
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01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Smith A.M., Klugman K.P.;
"Alterations in PBP 1A essential for high-level penicillin
                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae.";
Antimicrob. Agents Chemother. 42:2267-2273(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=#24/TJ25, #26/TJ29;
MEDLINE=98409715; PubMed=9736547;
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NCBI_TaxID=1313;
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Antimicrob. Agents Chemother. 42:1329-1333(1998).
EMBL, AF046231; AAC24696.1;
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087108;
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                                                                                                                         MEDLINE-93010977; PubMed-1396576; Martin C., Sibold C., Hakenbeck R.; "Relatedness of penicillin-binding protein la clones of penicillin-resistant Streptococcus South Africa and Spain.";
                    EMBO J. 11:3831-3836(1992).
EMBL; X67870; CAA48070.1; -.
InterPro; IPR001264; Transglycosyl
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
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Pfam; PF00905; Transpeptidase; 1.
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"Association of a Thr-371 substitution of penicillin-binding protein 1A with Streptococcus pneumoniae.";
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MEDLINE-98409715;
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NCBI_TaxID=1313;
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Q9EW42;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
PENICILLIN BINDING PROTEIN 1A
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087107;
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"Association of a Thr 371 substitution in a conse of penicillin-binding protein la with penicillin Streptococcus pneumoniae.";

Antimicrob. Agents Chemother. 42:2267-2273(1998).

EMBL; AB006877; BAA32073.1;
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Bacteria; Firmicutes; Bacillus/Clostridium
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  Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=#22/HA5;
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           Bacteria; Firmicutes;
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           Bacillus/Clostridium
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01-MAR-2001 (TIEMBLIE1. 16, Last sequence update)
01-DEC-2001 (TIEMBLIE1. 19, Last annotation updat
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
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Racteria; Firmicutes;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation
PENICILLIN BINDING PROTEIN 1A (FRAGMENT).
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                                                                                                                                                                                                                                                                             Antimicrob. Agents Chemother. 42:2267-2273(1998). EMBL; AB006870; BAA33066.L; ... InterPro; IPR001469; Transpeptdse. Pfam; PF00905; TranspeptIdase; 1.
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           Streptococcus mitis
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NCBI_TaxID=1313;
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  Bacteria;
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PubMed=9736547;
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 Bacillus/Clostridium group; Streptococcaceae;
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Amoroso A., Demares D., Mollerach M., Gutkind G., Coyette J.;
Amoroso A., Demares D., Mollerach M., Gutkind G., Coyette J.;
"All detectable high-molecular-mass penicillin-binding proteins
modified in a high-level beta-Lactam-resistant clinical isolate
streptococcus mitis.";
Antimicrob. Agents Chemother. 45:2075-2081(2001).
EMBL; AJ295856; CAC08466.1; -.
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001264; Transglycosyl.
InterPro; IPR0915; Transglycosyl; 1.
Pfam; PP00905; Transpeptidase; 1.
Pfam; PP00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
Q9EW44;
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SEQUENCE
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                                                                                                                                                                                                                               "Association of a Thr-371 substitution of penicillin-binding protein IA with Streptococcus pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                 087104
087104;
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STRAIN=#5/H31, #8/Z2,
MEDLINE=98409715; Publ
                                                                                                                                                                                                                                                                                                                   Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                      01.NOV-1998 (TrEMBLIEL. 08, Created)
01.NOV-1998 (TrEMBLIEL. 08, Last sequence update)
01.DEC-2001 (TrEMBLIEL. 19, Last annotation updat
PENICILLIN BINDING PROTEIN 1A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
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PubMed=9736547;
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Best Local Similarity
Matches 41; Conser
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Best Local Similarity
Matches 50; Conser
 Q93N72;
01-DEC-2001
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SEQUENCE 163 AA; 18464 M
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
PENICILLIN BINDING PROTE
                                                                                                                                                                                                                                                                     resistance in the Netherlands.";
Submitted (MAY-2000) to the EMBI
                                                                                                                                                                                                                                                                                                                                                        Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ403976; CAC20958.1; -.
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                     STRAIN=960027;
                                                                                                                        253 AQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLG
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                                                                                                           41 AQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLG
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163 AA;
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(TrEMBLrel. 16,
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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Lrel. 16, Last sequence update)
Lrel. 16, Last annotation update
PROTEIN 1A (FRAGMENT).
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18358 MW;
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18464 MW;
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1A (FRAGMENT).
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Pred. No. 3.6
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Best Local S
Matches 41
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J. Bacteriol. 180:1831-1840(1998).
EMBL; AJ002290; CAA05301.1; -
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00915; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
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Billot-Klein D., Legrand R., Schoot B., Gutmann L.;
"Acquisition of five high-Mr penicillin-binding prote during transfer of high-level beta-lactam resistance during transfer d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat)
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=B6;
MEDLINE=98196728; PubMed=9537382;
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                                                                                                          NSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLA
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Q9F2G7;
Q1-MAR-2001
01-MAR-2001
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EMBL; AJ40
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SEQUENCE
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Antimiorob. Agents Chemother. 45:2075-2081(2001).
EMBL; AJ295852; CAC08463.1; -.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                 "Molecular characterization of Streptococcus resistance in the Netherlands.";
Submitted (MAY-2000) to the EMBL/GenBank/DDB.
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InterPro; IPR001460; Transpeptdse.
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ETGYNLLTTGMDYYTNVDQEAQKHLWDIYN
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Lirel. 16, Last sequence update)
Lirel. 16, Last annotation updat
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                                                          EMBL; AE006596; AAK34416.1; InterPro; IPR001264; Transglycosyl. InterPro; IPR001460; Transpeptdse. Pfam; PF00912; Transglycosyl; 1. Pfam: PF00905; Transpeptidase; 1.
                                                                                                                                                          STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE-21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Addic D.J., Savic D.J., Savic C.
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an MI strain of Streptococcus
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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EMBL; AB006875; BAA32071.1; -.
InterPro; IPR001460; Transpeptdse.
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NCBI_TaxID=1314;
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MEDLINE=98409715;
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                                         ProDom; PD001895; Transglycosyl;
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INTERNAL REGION OF THE F
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; Z21809; CAA79874.1;
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PENICILLIN-BINDING PROTEIN 1
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Search completed: June 13, 2002, 08:50:23 
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                                                                                                                                       Query Match 3.0%; Score 20; DB 2; Length 310; Best Local Similarity 100.0%; Pred. No. 1.6e-11; Matches 20; Conservative 0; Mismatches 0; Indels
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SEQUENCE
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SEQUENCE FROM N.A.

STRAIN-63509, M11;

MEDLINE-98287565; PubMed-9624469;

MEDLINE-98287565; PubMed-9624469;

Smith A.M., Klugman K.P.;

Smith A.M., Klugman K.P.;

"Alterations in PBP 1A essential for high-level penicillin resistance
in Streptococcus pneumoniae.";

Antimicrob. Agents Chemother. 42:1329-1333(1998).

EMBL; AR046238; AAC24703.1; -.

EMBL; AR046238; AAC24703.1; -.

EMBL; AR046238; AAC24703.1; -.

EMBL; AR046238; AAC24703.1; -.

EMBL; PF00905; Transpeptidase; 1.
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O52744;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
NCBI_TaxID=1313;
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310 AA; 34354 MW; F8FCBACO0E7BF5FF CRC64;
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RESULT 1
US-08-961-083-2
; Sequence 2, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
Choi et. al.
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No.
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Maximum DB
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                                                                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
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and is
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STATE:
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                                                     Human Genome Sciences,
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US-08-481-435-6

US-08-645-511-4

US-08-600-993A-4

US-08-600-993A-24

US-08-600-993A-24

US-08-961-083-102

US-08-485-355B-40
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIIM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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APPLICATION NUMBÉR:
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING CONTROL OF THE CONTROL OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: IN 580/MAS/94 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: SE 9404072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 10-JUL-1CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Balganesh, Tanjo
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 60
      208
                                                                192
                                                                                                                          148
                                                                                                                                                                                       132
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                                                                                                                   EQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLTTGMDVYTNVDQ
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EQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLTTGMDVYTNVDQ
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10036-2787
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3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 0;
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US-08-245-511-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Pearce, Ba
APPLICANT: Tuomanen,
              MOLECULE TYPE:
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 PLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGARSTW 619
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                               TOPOLOGY:
                                                                                                            TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                           LENGTH:
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                                              amino acid
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                                                       320 amino acids
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Pearce, Barbara J
                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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Best Local Similarity

100.0%;

Query Match Best Local Similarity

36.8%;

Score 245; DB 2; Lo Pred. No. 1.3e-241;

Length 320;

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US-08-600-993A-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                               TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                 MOLECULE TYPE:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                                                                                                               TELEFAX:
                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/600,993A FILING DATE: 1-MAR-1996
                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
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                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYMSNGNYGMQ 135
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                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 Hackensack Avenue
                                                                320 amino acids
                                                                                                                                  201 343-1684
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                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
               protein
                                                                                                 4.
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                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOW PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Engant
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                           FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
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CITY: Ha
STATE: N
COUNTRY:
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                                   TYPE: amino acid TOPOLOGY: unknow
                                                                                                                            TELEPHONE: 201 343-1684
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                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Pearce, Barbara J
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                                     unknown
. peptide
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US-08-600-993A-24
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GENERAL INFORMATION:
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Best Local Similarity 100.0%; Matches 77; Conservative 0;
                                                                                                                              NFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
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                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 77 amino acids
                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS: Klauber & Jackson
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APPLICANT: Tuomanen,
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CLONE: SPRU42
                             MOLECULE TYPE:
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FRAGMENT TYPE:
                 ANTI-SENSE:
                                                                                                                                     TELEFAX: 201
TELEFAX: 133521
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                                                                                                                                               TELEPHONE: ZO1 343-1684
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 18-MAY-1994 CLASSIFICATION: 435
                                                               TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                             LENGTH:
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New Jersey
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Pearce, Barbara J
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NO
N-terminal
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Pred. No. 8.1e-71
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Best Local Similarity
Matches 77; Conserv
                             Best Local Similarity Matches 10; Conserv
                                                       Query Match
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                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: HP Vectra 48
OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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ORGANISM: Str
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CLONE: SPRU42
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 616 SSSSSSDSST 625
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                                                                                                                                TOPOLOGY: 11
                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                        LENGTH:
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7: USA
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9410 Key West Avenue
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                       36,373
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Pred. No. 0.026;
                               Mismatches
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RESULT 8

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US-08-485-3558-40

US-08-485-3558-40

JOS-08-485-3558-40

Sequence Wo. 6177075

REAL COMPANDED COMPANDERS: 57

COMPANDED COMPANDERS: 57

COMPANDERSEE: Floh: Nohbach Test Albritton & Herbert LLP
STREET: SOLIDENS:

LONGERSEE: Floh: Nohbach Test Albritton & Herbert LLP
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COMPANDERSEE: Floh: Solbach Test Albritton & Herbert LLP
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Sequence 2, Appli
Sequence 3973, Appli
Sequence 3973, Ap
Sequence 3705, Ap
Sequence 13423, A
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   US-10-072-851-13423
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Sequence 13423, A
Sequence 24, Appli
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Sequence 2567, Ap
Sequence 262, App
Sequence 10728, A
Sequence 355, App
Sequence 355, App
Sequence 355, App
Sequence 2706, Ap
Sequence 102, Appli
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Sequence 5073, Appli
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SUS-09-536-784-2
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US-09-536-784-2
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; GENERAL INFORMATION:
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Best Local Similarity
Matches 666; Conserv
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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/961,083 FILING DATE: OCT-30-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                              VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                     VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
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2 US-09-897-516-7108
6 US-60-215-161-7108
US-08-089-372-40
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Sequence 7108, Ap
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
TELEFAX: (
INFORMATION FOR SEQ
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                           REFERENCE/DOCKET NUMBER: PB340P3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                   APPLICATION NUMBER: 09/536,784
FILING DATE: <UNknown>
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/765,271 FILING DATE: 22-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MSDOS version SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville
STATE: Maryland
                                                                                                     REGISTRATION NUMBER: 41,971
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                                       TELEPHONE:
                                                                                                                             NAME: Michelle S. Marks
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RESULT 3
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID
US-09-765-271-2
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Best Local Sim
Matches 666;
         Sequence 2, Application US/09765272
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scier
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ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
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nes 666; Conserv
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
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LENGTH: 666 amino acids
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APPLICATION NUMBER: 08
FILING DATE: <Unknown>
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GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                                                                                                       VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYYNWDR
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                                                                                                       GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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STATE: Maryland
COUNTRY: USA
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301)
TELEFAX: (301) 3
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CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 3973
LENGTH: 719
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GENERAL INFORMATION:
APPLICANT: Lynn Do
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
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                                                                       GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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                                                                                                                                                                                                                                               SEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                         GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                                                 VSFGINQAVETNRDWGSTMKPITDYAPALEYGIYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                                                                                        TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                                                SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumoniae
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RESULT 5
US-09-107-433-3705
US-09-107-433-3705
; Sequence 3705, Application US/09107433
; GENERAL INFORMATION:
APPLICANT: Lynn A DOUCETTE-Stamm and Day
TITLE OF INVENTION: NUCLEIC ACID AND AM
SEQUENCES RELATING
NAME/KEY: misc_feature;
;
LOCATION: (B) LOCATION 1...721;
;
SEQUENCE DESCRIPTION: SEQ ID NO: 3705;
US-09-107-433-3705
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                                                                                                                                                                                             TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3705:
SEQUENCE CHARACTERISTICS:
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NAME: ATINICAL Peneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12,1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2,1997
                                                                                      ORIGINAL SOURCE:
ORGANISM: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5206 CORRESPONDENCE ADDRESS:
                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 100 B
                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                    LENGTH: 721 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                      pneumoniae
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AND AMINO ACID
LATING TO STREPTOCOCCUS PNEUMONIAE
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Best Local Sin Matches 665; Query Match

Local Similarity

84.8%; 99.8%;

Score 565; DB Pred. No. 0; 0; Mismatches

DB 15; 1;

Length 721; Indels

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Gaps

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Conservative

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RESULT 6
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                                         ; TYPE: PRT; ORGANISM: Streptococcus PCT-US02-03987-13423
                                                                                                                                                             Sequence 13423, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
                                                                         PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILLING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13423
LENGTH: 719
  Query Match
Best Local
                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
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Pred.
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No.
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           Length 719;
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AAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTG
                                                                                                                                                                                    LQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMA
                                                                                                                                                                                                                             NRDWGSTMKPITDYAPALEYGVYESTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
                                                                                                                                                                                                                                            NRDWGSTMKFITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
                                                                                                                                                                                                                                                                                                     EAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVET
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                                                                                                                                                                                                                                                                                                                                                                                                     TAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYISA
                                                                                                                                                                                                                                                                                                                                                                                                                    TAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYISA
                                                                                                               AAYAAFANGGTYYKPMYTHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLSYGTG
                                                                                                                                                                      LQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530;
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US-09-815-242-13423
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PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 2001-02-
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windc
SEQ ID NO 13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13423, App. GENERAL INFORMATION
                                                                                                                PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yamamoto, Robert T.
APPLICANY: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, APPLICANT: Ohlsen, K
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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Zyskind, Judith W.
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RESULT 8
US-10-072-851-13423
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APPLICANT: Xu, H.
APPLICANT: Foulkes
APPLICANT: Zamudio
APPLICANT: Haselbee
APPLICANT: Ohlsen,
APPLICANT: Zyskind
                                                                                                                                                                                                                                                                                  Sequence 13423, Application US/10072851 GENERAL INFORMATION:
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Best Local (
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          APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                APPLICANT:
APPLICANT:
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TYPE: PRT
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                                                                                                              Jiang, Bo
Boone, Charles
                                                                                                                                                  Trawick, John D.
Yamamoto, Robert T.
                                                                                                                                        Roemer,
                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                               Foulkes, J. Gordon
Zamudio, Carlos
                                                                                                                                                                                Wall,
                                                                                                                                                                                                                     Haselbeck, Robert
 ID NOS:
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Pred. No. 0;
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; TYPE: PRT
; ORGANISM: Streptococcus
US-10-072-851-13423
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SEQ ID NO 13423
LENGTH: 719
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Best Local Similarity
Matches 530; Conserv
           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                           APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELULIAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 45
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APPLICANT:
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                                                                                                   COUNTRY:
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CITY: Hackensack
 APPLICATION NUMBER:
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                                                                                                               New Jersey
                                                                                                                                        411 Hackensack
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Pred. No. 0;
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125 LTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYMSNGNYGMQ
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PLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGARSTW 603
                                                                 NRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
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ATTORNEY/AGENT INFORMATION:

FILING DATE: 19 CLASSIFICATION:

19930901

NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600

600-1-069

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Best Local
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                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: U$/08/116,541
FILING DATE: 1930901
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 320 amino acid
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Masure, H. Robert APPLICANT: Pearce, Barbara J. APPLICANT: Toumanen, Elaine
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136 TAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYISA 195
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NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRDWG 320
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                                                                                                                                                                                                  07601
                                                                                                                                                                                                                                            Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                             411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 amino acids
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                           Toumanen, Elaine
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                                                                                                                                                                                                                                                                              Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343-1684
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100.0%; Pr
100.0%; 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 320;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
         APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/00
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM
                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: SPRU42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 TTGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSS 299
                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 B
                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSS
                                                                                                                                                                                                                                                                                                                                  02354
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(781)893-8277
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Pred. No.
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US-09-107-532A-5667
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US-09-107-532A-5667
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Best Local Similarity 100.
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                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPAN: (781)893-8277
INFORMATION FOR SEQ ID NO: 5667:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1...823
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           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...823
SEQUENCE DESCRIPTION: SEQ ID NO: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
                                                                     FEATURE:
                                                                                                        ORIGINAL SOURCE:
                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: PC
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100.0%; O;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                 SEQ ID NO: 5667:
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Pred. No.
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US-09-634-238-262
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; ORGANISM: Lactobacillus rhamnosus US-09-634-238-262
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SOFTWARE: FastSEQ for
SEQ ID NO 229
LENGTH: 771
                                           SEQ ID NO 262
LENGTH: 771
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
Matches 14; Conserv
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                                                                   CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 110
                                                                                                                                                                                      APPLICANT:
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APPLICANT:
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                            LENGTH: 77
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Polynucleotides, TITLE OF INVENTION: them and methods
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                                                                                                                                                                                                                                                                                                                                                                                                         143 LQGGSTLTQQLIKL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LOGGSTLTQQLIKL 79
                                                                                                                                                                  Holland, Ross
O'Toole, Paul W.
Reid, Julian R.
Coolbear, Timothy
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Coolbear, Timothy
                                                                                                                                                                                                                                Christensson, Anna
                                                                                                                                                                                                                                                Dekker, James
                                                                                                                                                                                                                                                           Lubbers,
                                                                                                                                                                                                                                                                          Havukkala, Ilkka J.
Bloksberg, Leonard,
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O'Toole, Paul W.
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Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                         Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glenn, Matthew
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                                                                                                                            ON: Polynucleotides, ON: them and methods 11000.104301
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                                                                      for Windows Version 4.0
                                                                                                                                                                                                                                                            Mark W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%;
100.0%;
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100.0%; Pr
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Pred. No.
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Pred. No.
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for using
                                                                                                                                           for using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 771;
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APPLICANT: XU, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITA, 011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR TILING DATE: 2000-05-33

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Enterococcus faecalis PCT-US02-03987-10728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US02-03987-10728
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APPLICANT: Elitra Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10728
LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity 100.0%;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US02/03987 CURRENT FILING DATE: 2002-02-02
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NUMBER OF SEQ ID NOS:
                      PRIOR FILING DATE:
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Trawick, John D.
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pred. No.
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 10728
LENGTH: 778
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-10-072-851-10728
                                                                                                                                                                             US-09-134-000-4939; Sequence 4939, Application US/09134000A
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: MAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 4939
LENGTH: 789
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SEQ ID NO 10728
LENGTH: 778
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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CURRENT FILING DATE: 2002-02-08
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Zamudio, Carlos
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100.0%; Pred. No. 0.00056;
n. Mismatches 0;
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100.0%; Pred. No.
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                                                              Query Match
Best Local Similarity
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Best Local
                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
FILING DATE: 16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50533
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stodola, Robert
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
107 GGSTLTQQLIK 117
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                          83
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                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                           LENGTH:
                        GGSTLTQQLIK 78
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Similarity 100.0%;
14; Conservative 0;
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                                                     Conservative
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Knowles, David
Lonetto, Michael
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                                                                                                                                                      linear
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                                              1.7%; 5-
100.0%; Pr
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                                                                             Score 11;
                                                 Pred. No. 0.:; Mismatches
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0.00057;
hes 0;
                                                                 0.19;
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US-08-911-503A-535
; Sequence 535, Application US/08911503A
; GENERAL INFORMATION:

APPLICANT: Black, Michael
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; MOLECULE TYPE:
US-08-911-503-535
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                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/911,50
FILING DATE: 15 AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ginmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                            APPLICANT: Stodola, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 266 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                         APPLICANT:
                                                                                         APPLICANT:
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                                                                                                                                                                                                                                           107 GGSTLTQQLIK 117
                                                                                                                                                                                                                                                                           68 GGSTLTQQLIK 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SWEDELAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                        Knowles, David
Lonetto, Michael
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 amino acids
            SCOdola, Robert
VENTION: NOVEL PROKARYOTIC POLYNUCLEÓTIDES.
VENTION: POLYPEPTIDES AND THEIR USES
EQUENCES: 713
                                                                                                                    Hodgson, John
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Lonetto, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...ER: US/08/911,503
: 15-AUG-1997
ON: 536
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                                                                                                                                                                                                                                                                                                                        1.7%; Score 11;
100.0%; Pred. No.
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. 0.19;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: F
US-08-911-503A-535
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US-09-417-507-35782
                                                                                                                                                 ; ORGANISM: A.fumigatus
US-09-417-507-35782
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 35782
LENGTH: 314
                                                                                                                                                                                                                                                                                             Sequence 35782, Application US/09417507
GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
                                                              Query Match
Best Local Similarity
Matches 11; Conserv
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Best Local S
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                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,503A
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                             616 SSSSSSSSTS 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 GGSTLTQQLIK 117
148 SSSSSSDSSTS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 GGSTLTQQLIK 78
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/024,022 FILING DATE: 16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
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                                                                Conservative
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                                                                              1.7%;
100.0%;
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100.0%; Pr/
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                                                              0;
                                                                            Score 11; DB 18; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11; DB 13; Length 266; Pred. No. 0.19;
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                                                              Mismatches
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                                                                                            Length 314;
                                                              Indels
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RESULT

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RESULT 25
US-09-377-465A-2
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TYPE: PRT
GRGANISM: Streptococcus pneumoniae
US-09-377-465-2
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4219
: Sequence 2, Application US/09377465A
GENERAL INFORMATION:
APPLICANT: HOSKINS, JOANN
APPLICANT: Jaskunas, Stanley R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-377-465-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/100,887
EARLIER FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 60/111,862
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09377465
GEMERAL INFORMATION:
APPLICANT: Hoskins, Joann
APPLICANT: Jaskunas, S. Richard
APPLICANT: Zhao, Genshi
APPLICANT: Chao, Genshi
APPLICANT: Rockey, Pamela
TITLE OF INVENTION: Novel Penicillin Binding Protein From Streptococcus
TITLE OF INVENTION: pneumoniae
FILE REFERENCE: X12498
CURRENT FILING DATE: 1999-08-19
CURRENT FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserv
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SEQ ID NO 4219
LENGTH: 820
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Best Local :
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR ETILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                   176 GGSTLTQQLIK 186
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100.0%; Pred. No. 0.
ive 0; Mismatches
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. 0.54;
                                                                                                                                                                                                                                                                                              Length 821;
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RESULT 26
US-09-107-433-4760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4760, Application US/09107433
GENERAL INFORMATION:
GENERAL INFORMATION:
DOucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROCKEY, PAMELA K
TITLE OF INVENTION: PNEUMONIAE
FILE REFERENCE: X12498 Sequence List
CURRENT APPLICATION NUMBER: US/09/377,465A
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 60/100,887
PRIOR EILING DATE: 1998-09-23
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                                                                                                                                                      TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4760:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 GGSTLTQQLIK 186
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 GGSTLTQQLIK 78
                                                       LENGTH: 834 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
FEATURE:
                                      ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, Genshi
               ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...834;
SEQUENCE DESCRIPTION: SEQ ID NO: 4760:
US-09-107-433-4760
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, NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
US-09-621-976-7706
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SOFTWARE: Patent.pm
SEQ ID NO 7706
LENGTH: 76
TYPE: PRT
                                                                                                                           PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 24929
SEQ ID NO 24929
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24929, Application US/09834366 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                        APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: 81.US2.REG
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/834,366 CURRENT FILING DATE: 2001-04-13
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APPLICANT:
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NAME/KEY: UNSURE
LOCATION: 72
OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                        FEATURE:
                                                                                                              LENGTH:
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100.0%; Pred. No.
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US-09-834-366-24929

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US-60-147-499-7706
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; LOCATION: 72
; OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
US-09-834-366-24930
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                                                                                            CURRENT APPLICATION (NUMBER: US/60/147,499 CURRENT FILING DATE: 1999-08-05 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 7706 LENGTH: 76
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LENGTH: 76
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Best Local (
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APPLICANT:
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OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
-60-147-499-7706
                                                                                                                                                                                                           APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/834,366 CURRENT FILING DATE: 2001-04-13 PRIOR APPLICATION NUMBER: US 60/197,873 PRIOR FILING DATE: 2000-04-18
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81.US2.REG
                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B.
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                                              NAME/KEY: UNSURE
                                                                FEATURE:
                                                                           ORGANISM: Homo sapiens
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Dumas Milne Edwards,
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Pred. No.
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa = Ala,Pro,Ser,Thr
US-60-197-873-24929
                                                                      ; LOCATION: 72
; OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
US-60-197-873-24930
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SOFTWARE: Paten
SEQ ID NO 24929
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SEQ ID NO 24930
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ESTs and Encoded Human Proteins FILE REFERENCE: 81.US1.PRO
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CURRENT FILING DATE: 2000-04-18
                                                                                                                                                              LENGTH: 76
TYPE: PRT
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NAME/KEY: UNSURE
                                                                                                                                               ORGANISM: Homo sapiens
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Tanaka, Hiroaki
Dumas Milne Edwards, Jean Baptiste
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Tanaka, Hiroaki
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100.0%; Pred. No.
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             1.5%;
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Score 10; DB Pred. No. 0.5 0; Mismatches
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               DB 26;
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US-09-536-784-102
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                                                                                               Sequence 102, Application US/09765271
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 102, Application US/0
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 616 SSSSSSSST
                                                                                                                                                                                                                                                                  38
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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            STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/961,083 FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 Key West Avenue CITY: Rockville
COUNTRY:
                               CITY: Rockville
                                               STREET: 9410 Key West Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/536,784 FILING DATE: 30-Oct-1997
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Pred. No.
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0.78;
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RESULT 35
US-09-765-272-102
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Best Local :
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
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                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4m

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272

FILING DATE: 22-Jan-2001

CLASSIFICATION: CUnknown>
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/961,083 FILING DATE: OCT-30-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/765,271 FILING DATE: 22-Jan-2001 CLASSIFFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 488
                                                                           APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                             CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
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RESULT 37
US-60-191-637-33895
; Sequence 33895, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
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Best Local S
Matches 10
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SEQ ID NO 34311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-01-12 PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
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PRIOR APPLICATION NUMBER: 60/161,932
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
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                                                                                                                                                                                              617 SSSSSDSSTS 626
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les 10; Conserv
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10; Conserv
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STRANDEDNESS: sir
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                               1.5%; Score 10; DB 20; 100.0%; Pred. No. 0.84;
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Pred. No.
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US-09-621-976-5866
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                                                                                                                                                                                       Sequence 5866, Application US/60147499 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patent.pm
SEQ ID NO 5866
NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 5866
LENGTH: 130
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Best Local
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Best Local Similarity
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                                                              APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/80/147,499
CURRENT FILING DATE: 1999.08-05
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CURRENT FILING DATE: 2000-07-21
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
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TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/278,650
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PRIOR APPLICATION 1
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OR APPLICATION NUMBER: PCT/US00/06822
OR FILING DATE: 2000-03-16
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APPLICATION NUMBER: PCT/US00/06014
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APPLICATION NUMBER: PCT/US00/06013
FILING DATE: 2000-03-09
APPLICATION NUMBER: PCT/US00/06049
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FILING DATE: 2000-03-16
APPLICATION NUMBER: PCT/US00/06830
FILING DATE: 2000-03-16
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APPLICATION NUMBER: PCT/US00/06057
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APPLICATION NUMBER: PCT/US00/06042
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APPLICATION NUMBER: PCT/US00/09066
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APPLICATION NUMBER: PCT/US00/09068
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APPLICATION NUMBER: PCT/US00/08981
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APPLICATION NUMBER: PCT/US00/08982
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APPLICATION NUMBER: PCT/US00/08983
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APPLICATION NUMBER: PCT/US00/07726
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APPLICATION NUMBER: PCT/US00/09070
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APPLICATION NUMBER: PCT/US00/07722
FILING DATE: 2000-03-23
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APPLICATION NUMBER: PCT.
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FILING DATE: 2000-03-22
APPLICATION NUMBER: PCT/US00/07526
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APPLICATION NUMBER: PCT/US00/07525
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APPLICATION NUMBER: PCT/US00/07534
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PRIOR APPLICATION NUMBER: PCT/US00/26323
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: PCT/US00/26337
PRIOR FILING DATE: 2000-00-26
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: PCT/US00/26324
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APPLICATION NUMBER: US 60/125,360
FILING DATE: 1999-03-19
APPLICATION NUMBER: US 60/138,626
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APPLICATION NUMBER: US 60/124,143
FILING DATE: 1999-03-12
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FILING DATE: 1999-12-03
APPLICATION NUMBER: US 60/124,096
FILING DATE: 1999-03-12
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APPLICATION NUMBER: US 60/124,145
FILING DATE: 1999-03-12
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FILING DATE: 1999-03-12
APPLICATION NUMBER: US 60/166,989
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FILING DATE: 1999-03-12
APPLICATION NUMBER: US 60/167,061
FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/124,142
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APPLICATION NUMBER: US 60/138,574
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APPLICATION NUMBER: US 60/168,665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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APPLICATION NUMBER: US 60/125,359 FILING DATE: 1999-03-19
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PRIOR APPLICATION NUMBER: 09/687,527
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 892
SOFTWARE: Custom
SEQ ID NO 504
LENGTH: 263
TYPE: PRT
ORGANISM: Homo sapiens
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                                             Query Match
Best Local Similarity
Watches 10; Conserva
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                                                                                                                                              SEQ ID NO 504
LENGTH: 263
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: HYSEG, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-115/ 785
CURRENT APPLICATION NUMBER: PCT/US01/27760A
CURRENT FILING DATE: 2001-10-11
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Best Local Similarity
Watches 10; Conser
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Matches
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PRIOR APPLICATION NUMBER: US 60/126,051
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/169,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US01/27760 CURRENT FILING DATE: 2001-10-11
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                                                                                                                                                                                                               NUMBER OF SEQ ID SOFTWARE: Custom
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/687,527 PRIOR FILING DATE: 2000-10-12
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SSSSSSDSST 227
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100.0%; Pred. No. 1.
tive 0; Mismatches
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Pred. No.
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RESULT

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RESULT 45
US-09-287-788-3
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Sequence 3, Application US/09287788B GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine I
APPLICANT: Masure, H. R.
TITLE OF INVENTION: POLYPEPTIDE CO
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Best Local Similarity
Matches 10; Conserv
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LENGTH: 284
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LENGTH: 263
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Best Local :
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APPLICANT: Wizemann, Theresa
APPLICANT: Mizemann, Theresa
APPLICANT: Masure, H. R.
APPLICANT: Johnson, Lesile S.
APPLICANT: Koenig, Scott
TITLE OF INVENTION: POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
TITLE OF INVENTION: CHOLINE BINDING PROTEIN A TRUNCATE, VACCINE DERIVED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
FILE REFERENCE: 1340-1-017
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APPLICANT: Bush, Angie
APPLICANT: Heichman, Karen
APPLICANT: Heichman, Karen
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
FILE REFERENCE: 2318-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/056,019A CURRENT FILING DATE: 1998-04-07 NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/185,080
PRIOR FILING DATE: 2000-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
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Similarity 100.0%;
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POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
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100.0%; Pr
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b; Pred. No. 1.9
0; Mismatches
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SEQ ID NO 3
LENGTH: 28
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 406
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
                                                                                                           APPLICANT: Tuomanen, Elaine I
APPLICANT: Masure, H. R.
TITLE OF INVENTION: POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
TITLE OF INVENTION: CHOLINE BINDING PROTEIN A TRUNCATE, VACCINE DERIVED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
FILE REFERENCE: 1340-1-017N
TELER REFERENCE: 1340-1-017N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tuomanen, Elaine I
APPLICANT: Wizemann, Theresa
APPLICANT: Masure, H. R.
APPLICANT: Masure, H. R.
APPLICANT: Johnson, Lesile S.
APPLICANT: Koenig, Scott
TITLE OF INVENTION: POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
TITLE OF INVENTION: CHOLINE BINDING PROTEIN A TRUNCATE, VACCINE DERIVED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
FILE REFERENCE: 1340-1-017
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FITLE OF INVENTION: THEREFROM AND USES THE
FILE REFERENCE: 1340-1-017N
CURRENT APPLICATION NUMBER: US/09/287,788B
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 60/080,878
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 39
                   CURRENT APPLICATION NUMBER: US/09/287,788B
CURRENT FILING DATE: 199-04-07
PRIOR APPLICATION NUMBER: 60/080,878
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS:
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100.0%; Pred. No.
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CURRENT APPLICATION NUMBER: US/09/056,019A; CURRENT FILING DATE: 1998-04-07; NUMBER OF SEQ ID NOS: 39; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 24; LENGTH: 428; TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-056-019-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 406
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-287-788-1
; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-287-788-24
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US-09-287-788-24
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                                                          SOFTWARE: Pat
SEQ ID NO 24
LENGTH: 428
                                                                                                                                                                                                                                        Sequence 24, Application US/09287788B
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine I
APPLICANT: Masure, H. R.
TITLE OF INVENTION: POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
TITLE OF INVENTION: CHOLINE BINDING PROTEIN A TRUNCATE, VACCINE DERIVED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09056019A GENERAL INFORMATION:
                                                                                                                                                                          FILE REFERENCE: 1340-1-017N

CURRENT APPLICATION NUMBER: US/09/287,788B

CURRENT FILING DATE: 1999-04-07

CURRENT FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnson, Leslie S.
APPLICANT: Koenig, Scott
TITLE OF INVENTION: POLYPEPTIDE COMPRISING THE AMINO ACID OF AN N-TERMINAL
TITLE OF INVENTION: CHOLINE BINDING PROTEIN A TRUNCATE, VACCINE DERIVED
TITLE OF INVENTION: THEREFROM AND USES THEREOF
FILE REFERENCE: 1340-1-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tuomanen, Elaine APPLICANT: Wizemann, Theresa
                                                                                                                                           PRIOR APPLICATION NUMBER: 60/080,878 PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Masure, H. R.
                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||||||
113 SSSSSSDSST 122
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                                                                                                     PatentIn Ver. 2.0
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Search completed: June 13, 2002, 08:48:47 Job time: 243 sec
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; TYPE: PRT
; ORGANISM: Corypebacterium glutamicum
US-09-605-703B-1256
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 1256
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/142,764 PRIOR FILING DATE: 1999-07-08
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                                                                                         59 SSSSSSDSST 68
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Zelder, Oskar
                                                                                                                                                             1.5%; Score 10; DB ilarity 100.0%; Pred. No. 2.: Conservative 0; Mismatches
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Maximum
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Perfect score:
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                                                                                                     Sequence 2, Application US/08961083
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
            CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
STREET: 9410 Key West A
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
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COMPUTER READABLE FORM:
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US-09-769-744A-122

US-08-961-083-1.02

US-10-1.05-299-4083

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ US-08-961-083-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
                                                                                                                                                                                                                                         GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD 420
                                                                                                                                                                                                                                                                                                                   VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
               AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR 600
                                                                                                                                                                                                                        GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                                                                                                                                                                                                                                                                                                          TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                                                                                                                                                                                                                           TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
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AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
                                                                                                                                              KKYGASSEKMAAAYAAFANGGTYYKPMYTHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                                                                                                                                                                                                                VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
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TELEPHONE: (301) 309-000
(301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
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Pred. No. 0;
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Length 110;

Indels

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21122MO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT APPLICATION NUMBER: PCT/GB99/02452
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-3-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102, Application US/08961083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 122, Application US/09769744A GENERAL INFORMATION:
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LENGTH: 821
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Le Page, Richard WF APPLICANT: Wells, Jeremy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 GGSTLTQQLIK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GGSTLTQQLIK 78
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                     CURRENT APPLICATION DATA:
                   ATTORNEY/AGENT INFORMATION:
                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQPAQP 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STWNSPAPQQPPSTESSSSSSSSSSTSQSSSTTPSTNNSTTINPNNNTQQSNTTPDQQNQN 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                       APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>
                                                                                             APPLICATION NUMBER: US/08/961,083 FILING DATE: 30-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                           STATE: Maryland
                                                                                                                                                                                                                                                                         ZIP: 20850
Brookes,
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100.0%;
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Pred. No.
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0.073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                             APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3150
LENGTH: 602
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID US-08-961-083-102
                                                                                                                                                                                                                                                                                                                            US-60-360-039-3150; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-10-105-299-4083
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                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4083
LENGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen, et. al TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
             ORGANISM: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          149 SSSSSSSST 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 SSSSSSDSST 625
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10; Conserv
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10105299
                                                                                                                                                                                                                                                                                                                          Application US/60360039
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Length 194;

Indels

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Gaps

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PLANTS FOR PRODUCTION OF

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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-991-262-40
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US-09-991-262-40
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; LOCATION: (1)..(602)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-3150
                                                                                                                                                                                                                     NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: 910 277799
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application US/09991262'
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.5%;
Best Local Similarity 100.0%;
                                                             Query Match
Best Local Similarity
                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 ESSSSSSDSS 624
617 SSSSSDSSTS 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,262
FILING DATE: 20-Nov-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/234,238
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: US 08/485,355
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                     1.5%; Score 10; DB 5; illarity 100.0%; Pred. No. 1.2; Conservative 0; Mismatches
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Pred. No. 0.48;
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                                                                               Length 1704;
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                                         Indels
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                                         0;
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Search completed: June 13, 2002, 08:49:37 Job time: 228 sec

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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq
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Perfect score:
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length: 2000000000
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   100.0
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63.4
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1: /SIDS1/gcgdata/
2: /SIDS1/gcgdata/
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 13, 2002, 08:40:34 ; Search time 34.61 Seconds (without alignments) 2137.392 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen
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                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
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cus a	139	19	269		æ	ü
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Mycobacterium tube	AAG81232	22	810		419	37
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pylori ORF 06e	5557	18	660		625	5
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eisseria gono	56	21	805	18.2	635.5	ω
S. pneumoniae peni	AAW44849	19	731	8	636	2

## ALIGNMENTS

(first entry)

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pneumoniae SP001 protein.

WPI; 199 N-PSDB; Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Choi GH, Hromockyj A, 31-OCT-1996; 30-OCT-1997; WO9818930-A2 Streptococcus pneumoniae (HUMA-) HUMAN GENOME SCI INC. 07-MAY-1998. 1998-272224/24. DB; AAV27323. 96US-0029960 97WO-US19422 Johnson ĽS, Kunsch CA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sol. derivs. of bifunctional penicillin binding protein opt. lack transglycosylase activity, useful to identify for antibodies or cpds. which bind BPBPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transglycosylase; transpeptidase; identi antibiotic resistant; bacteria; soluble X-ray crystallography; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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01-JUL-1994;
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SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                  VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
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                                                                      vymsngnygmqtaaqnyygkdlnnlslpqlallagmpqapnqydpyshpeaaqdrrnlvl
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94IN-0000580.
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Pred. No. 2e-233;
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                GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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                                                                                                                                                                    AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
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                                                    VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
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2000us-257931P.
2001us-269308P.
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2000US-207727P.
2000US-242578P.
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Xu HH;
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N-PSDB; AAS55689.
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26-MAY-2000;
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22-DEC-2000;
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prokaryotic cellular proliferation, their use in identifying the prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus and Enterococcus faccalis. The preumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The preumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also used in Foreitian of protential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins.

The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                              The invention relates to antisense inhibitors of genes
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Pred. No. 2.1e-233
 comprise sequences of antisense
                               ID No 13423; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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99.4%;
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Best Local Similarity 99.43
Matches 662; Conservative
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AAY56106;

AAY56106 RESULT

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                           492 RNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLT
                                                                                                                                                                                                                                                                                                                           552 PLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQP
                                                                                                                                                                                                                                                                                                                                                                                                       EAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVET
                                                                                                                                                                                                                             432 AAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTG
                                                                         312 NRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis cellular proliferation protein #422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU35135 standard; Protein; 778
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2000US-206848P.
2000US-207727P.
2000US-242578P.
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2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Seq ID No 10728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis.
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22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A; transpeptidase encoding region; TER; antibiotic resistance; diagnosis; detection; identification; pneumococcal meningitis.
654 stwsspapgqppstesssssdsstsgsssttpstnnstttnpnnntggsnttpdggngn 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2208; DB 20;
Pred. No. 6.6e-146;
; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du Plessis M;
                                                                                                                                                                     AAY56106 standard; Protein; 420 AA.
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99.0%;
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                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-601770/51.
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                                   661 PQPAQP 666
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pqpaqp 719
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useful for
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Matches 416;
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(SAME-)

Carr GJ;

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Sequence

Query Match

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protein; pbpla; plpA; expl; exp3; pad1;

(first entry)

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virulence determinant; permease like protein; permease like protein; penicillin binding protein 1A; pyruvate oxidase; regulatory element; acellular vaccine; antibody.
                                                                     Streptococcus pneumoniae strain SPRU42 Exp2.
                                                                                                                                                                                                                                                                                                                                                                                                               wel gene fragments encoding specifically of S. pneumonia
                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                           Masure HR, Pearce BJ,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-115448/15.
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                                                                                               Exp2; export
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                                          14-FEB-1996
                                                                                                                                                                                                                                                                          01-SEP-1993:
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                AAR70153;
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                                                  The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
invention is also useful for the identification of potential new targets for antibitic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                       201 vymangfygmetaaenyygkhlseldlpqtallagmpqapnsydpytkpdtakerrdvvl 260
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                                                                                                                                                                                                                                                                                                            81 klydinneifedlgaekreliqpndvpqllkdaivsvedrrfykhigvdpiriigsalsn 140
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                                                                                                                                                                                                                                Query Match 50.3%; Score 1751; DB 22; Best Local Similarity 51.4%; Pred. No. 1.3e-113; Matches 347; Conservative 125; Mismatches 193;
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encoding specific bacterial exported proteins pneumoniae, useful as vaccines

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Tuomanen

ROCKEFELLER

94WO-US09942. 93US-0116541. 94US-0245511.

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sequence can be inserted into an expression vector (preferrably a bacterial expression vector) to provide for high levels of expression of the protein. The protein can then be used in the production of an acellular vaccine. These vaccines are used to provide protection from Gram positive bacterial infection. Antibodies against export proteins
                                                This sequence represents exp2. The DNA encoding this sequence is identical to that for ponA which encodes penicallin-binding protein IA (PBPIA). This sequence is involved in adhesion of bacteria to target cells. This sequence is an exported protein of S.pneumoniae. Export proteins are the proteins in pathogenic bacteria that are virulence determinants. Other export proteins include plpA (see AAR70152), exp3, and pad1 (encoded by the sequence shown in AA083259). This
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                                                                                                                                                                                                                                                                                                                                                                                     can be used for diagnosis of infection and in passive immune therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1621; DB 16;
Pred. No. 4.3e-105;
0; Mismatches 1;
Claim 35; Page 88-9; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.7
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AAR70153 standard; Protein; 320 AA.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomona aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                              242 GMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNV 301
|: ||||: :||| |:||||:|||:||:||:||:||: ||
298 glkvytnintdaqkqlydiynsdtylaypnnelqiastimdatngkvlaqlggrhqneni 357
               178 ymgngnygmrttaksyfgkdlkelsiaglallagipqaptqydpyknpesagtrrntvlg 237
                                                                                                                                                                                                                                                            :| || ::|::|| || ::|| 38 gmyqdkniskkeydqavatpvtdglkelkqkstypkymdnylkqvisevkqktgkdifta
                                                              EMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLTT
                                                                                                                                                                                                                                   SFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDRG
= = ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #562.
                                                                                                                                                                                                                                                                                                                          362 YFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSI 406
                                                                                                                                                                                                                                                                                                                                                                   418 ymgwmsmqtaiqqsrnvpavraleaagldeaksfleklgiyypem 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Seq ID No 5782; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL, Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU34286 standard; Protein; 727
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611495/70.
N-PSDB; AAS52145.
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22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus agalactiae) amino acid sequences of the invention. S. agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and maningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 QSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 YMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  245 tgmdvytnvdqeaqkhlwdiyntdeyvaypddelqvastivdvsngkviaq1garhqssn 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61
                                                                                                                                                                                                                                                                                                                                                                                         Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis; meningitis; neonate; antigenic; vaccine; infection; genital tract; capsid polysaccharide vaccination.
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                                                                                                                                                                                                                                                                                                                                                     Group B Streptococcus antigenic protein, ID-122.
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62.0%; Pred. No. 1e-86;
Live 73; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SB;
                                                                                                                                                                                                                      AAU03646 standard; Protein; 462 AA.
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                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 62.0;
Matches 251; Conservative
                                                                                           305 vsfgingavetnrdwg 320
                                                                   301 VSFGINQAVETNRDWG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-316444/33.
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Staphylococcus aureus cellular proliferation protein #1354.
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23-OCT-2000;
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22-DEC-2000;
                                                                                                                                                21-MAR-2000;
                                                                                                                                                                                                                                                           Haselbeck R,
                                                                                                                                                                                                                                                                     Yamamoto RT,
                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                         22;
programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                      346
                                                                                                                                                                                          60 NLQSN-SLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118
                                                                                                                                                                                                                                     179 VLSEMKNQGYISAEQYEKA-----VN-TPITDGLQSLKSASNYPAYMDNYLKEVIN 228
                                                                                                                                                                                                                                                                                                                                                                                                                            427
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                                                                                                                                                                                                                                                                   NKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNL 178
                                                                                                                                                           Gaps
                                                                                                                                                                              1 KIYDNKNQLIADL-GSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLR 59
                                                                                                                                                                                                                                                                                 ::| | | | : | || : |||::|| | ||:|| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 KVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                NYPGTNTPVYNWDRGYFGNITLQYALQOSRNVPAVETLNKV----GLNRAKTFLNGLGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 YP-SIHYSNAISSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 FSNVGTRAMKETTAYMMTDMMK-TVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 SNP----EDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQPPSTESSSSSSDSSTSQSSST
                                                                                                                                                                                                                                                                                                                                                         Q--VEEETGYNLLTTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 486 yegdigpsevlggsase----fsptglasafaaianggtynnahsigkvytrdgetie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 ydhtshkamsdytaymlaemlkgtfkpygsayghgvsgvnmgaktgtgtygaety----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 TSQFVAPDEL----FAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 -sqynlpdnaakdvwingftpqytmsvwmgfsk------vkqy-----g
                                                                                                                                                         81;
                                                                                                                                    Length 727;
                                 essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                                                                                                                                       Mismatches 261; Indels
                                                                                                                                  DB 22;
                                                                                                                                Score 817.5; DB 2
Pred. No. 1.8e-48;
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                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                         Conservative 128;
                                                                                                                                  23.5%; 32.1%;
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                                                                                                                                              Similarity
                                                                                                   727 AA;
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                                                                                                                                                        Matches 222;
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                                                                                                   Sequence
                                                                                                                                   Query Match
                                                                                                                                              Best Local
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aucues, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organism. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the printed specification, but was obtained in electronic mat directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Antisense; prokaryotic cellular antibiotic; antibacterial; drug
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
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                                                                                             Staphylococcus aureus
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N-PSDB; AAS55043.
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Best Local Similarity
Matches 222; Conserv
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Tettelin H,
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Scalato E, Scarselli
VLSEMKNQGYISAEQYEKA------VN-TPITDGLQSLKSASNYPAYMDNYLKEVIN
        KVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPY
                                                                    347 NYPGTNTPVYNWDRGYFGNITLQYALQQSRNVPAVETLNKV----GLNRAKTFLNGLGID
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                             229 Q -- VEEETGYNLLTTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNG
                                                                                                                                                                                 TSQFVAPDEL----FAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEG
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Ratti G,
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Rappuoli R,
                                                                                                                                                                                                                                                                                               AAY75603 standard; Protein; 805 AA
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98US-0098994.
98US-0099062.
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25-FEB-1999;
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ55473 represent pCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                       Claim 2; Page 1270; 1453pp; English.
                                                                                                                                                                                  vaccines and diagnostics
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                                                                                                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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---kdawfvgfnpd 676
                       538 YSMAVWTGYSN-RLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLY-RNGEFVF 595
                                        596 K----NGARSTWNSPAPQQPP-----STESSSSSSDSSTSQSSTTPSTNNST 639
                                                                                              737 kermvtdpgltldnsgiapqpsrrakeddggaaeggrqaaddevrqdmqetpvlpsnt 794
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Scalato E, Scarselli
                                                                                                                                                                                                                                       Neisseria meningitidis ORF 791 protein sequence SEQ ID NO:2678
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632 ykimqdvvrvgtargaaalgrtdiagktgttn-----dn--
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Rappuoli R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ54364
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                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1999;
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Tettelin H,
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31-JUL-1998;
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09-OCT-1998
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09-0CT-1998
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                                                                                                         62 QSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                              236 nnmleekmitvggrdgalneel-----hyerfvrkidgsalyvaemvrgelyek 284
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                                                                                                                                                                                                                                        121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                                                                               285 ygedaytggfkvyttvradhqkvatealrkalrnfdrgssyrgaenyidlsksedveetv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 nnekmgedrirrgavirvknnggrwavvqepllqgalgsldaktgavralvggydfhskt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 INQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN-----TPVYNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 DRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 SDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE-----FSNVGTRAMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 rnayimykimqdvvrvgtargaaalgrtdiagktgttn-----dn-----kdawf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532 AGYTRKYSMAVWTGYSN-RLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLY-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 NGEFVFK----NGARSTWNSPAPQQPP-----STESSSSSSSSSSTSQSSTTPST
                                                                                                                                                                                                                                                                                                                         SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDN-----YLKEVINQ-VEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 TTAYMMTDMMKTVLTYGTGRN-AYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --HLWDIYNTDEYVAYPDDELQVASTIVDVSNGK-VIAQL-GARHQS------
                                         Indels 194;
  Length 805;
Query Match 18.3%; Score 638; DB 21; 1
Best Local Similarity 26.0%; Pred. No. 7.1e-36;
Matches 204; Conservative 125; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                   234 TGYNLLTTGMDVYTNVDQEAQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae penicillin-binding protein PBP-Nv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW44849 standard; Protein; 731 AA
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54431 represent polyneptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55431 represent polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55431 represent polypeptides. The polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing in the neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarselli M;
528 mpeahfisrienasgqviashknsqkrvidksvadkmtsmmlgtftngtgissspadyvm 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mora M;
                                   AGKTGTSNYTDEE1ENHIKTSQFVAPDELFAGYTRKYSMAVWTGY----SNRLTPLVGN
                                                                                                                                            ------pytpg
                                                                                                       557 GLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQPPSTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                       agktgtt----eavfnpeyts-----dqwvigytpdvvishwlgfpttdenhylagstsn
                                                                                                                                                                                                                                                                                                                                                                                                                gonorrheae ORF 791 protein sequence SEQ ID NO:2676.
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Scalato E, S
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Ratti G,
                                                                                                                                                                                                    |: ::: |: :: |: stftvenaykqngiapantkrqvqtndnsqtddn
                                                                                                                                                                                SQQTNNNATTTRNNSTTRQSSSTSQSSSSS 713
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, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                        AAY75601 standard; Protein; 805
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98US-0098994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrheae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-062150/05.
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Tettelin H,
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02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the Streptococcus pneumoniae penicillin-binding protein, designated PBP-NV, of the invention. The protein is useful in screening assays for compounds that bind to PBP-NV or inhibit the . transglycolase or trans-peptidation activity of PBP-NV. Such compounds would be useful as antibacterial agents for treating S. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- MAAAYAAFANGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||||:|||| | | | |||: |||:| :||:| ||:|| ||:| tagrsgggstitqqlaknayls---qdqtverkakefflalelskkyskeqiltmylnna 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 YMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYNLLTTGMDVYTNVDQEAQKHLWDIY-NTDEYVAYPDDEL-QVASTIVDVSNGKVIAQL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NYPGTNT----PVYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGI 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYKPMYIHKVVFSDGSE-KEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQ 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPY----
                                                                                                                                                                                                                                                                                                                                                            Recombinant Streptococcus pneumoniae penicillin-binding protein useful in screening assays for antibacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 142;
                                                                                                                                                                                                                                                        Rosteck PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.3%; Score 636; DB 19; Length 731; 27.7%; Pred. No. 8.5e-36;
                                                                                                                                                                                                                                                      Rockey PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252;
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     trans-peptidation activity; infection; therapy
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                                                                                                                                                                                                                                                        Norris FH,
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 19-21; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108;
                                                                                                                                                                                 96US-0731716.
                                                                                                                                                97EP-0308288.
                                                                                                                                                                                                                                                        Hoskins JA, Jaskunas SR,
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                                          pneumoniae.
                                                                                                                                                                                                                     (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AA;
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                                        Streptococcus
                                                                                                                                                17-0CT-1997;
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                                                                                                             22-APR-1998
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Matches 192;
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                                                                                                                                                                                                                                                                            Zhao G;
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                                                                                                                                                                                                                                                                                                                   410 virvknnggrwavvqepllqgalvsldaktgavralvggydfhskt---fnravqamrqp 466
                                                                                                                                                                                                                                                                                                                                        369
                                                                                                                                                                                                                                                                                                                                                989
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                                                                                                                   OSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                       VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                         370 YALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLTYGTGRN-AYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       742 tdpglmldnsgiapg--psrrakeddeaaveneqqgrsdetrqdvqetp---vlpsntds 796
                                                               Gaps
                                                                                 61
                                                                                                                                                               SEMKNOGYISAEQYEKAVNTPI--TDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNL
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vaeaysvfanggyrvsshvidkiydrdgrlraqmqplvagqnapqaidprnayimykimq
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                                                                                                                                                                                                    MTH------
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350 glytvdkmvpavyldvtkknvviqlpggrrvaldrralgfaaravdnekmgedrirrga
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                                            Query Match 18.2%; Score 635.5; DB 21; Length 805; Best Local Similarity 26.4%; Pred. No. 1.1e-35; Matches 207; Conservative 120; Mismatches 287; Indels 169;
                                                                                                                                                                                                                                                                  -AYPDDE-
may also be used in gene therapy protocols.
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This sequence is a H. pylori cell envelope inner membrane protein

involved in outer membrane and cell wall synthesis. The protein may be

used in a vaccine to prevent or treat, pylori infection or to identify

H. pylori polypeptide binding compounds, useful as potential H. pylori

Ilfe cycle activators or inhibitors. The DNA and probes derived from it

may be used for the identification of H. pylori in a sample and the

diagnosis of H. pylori infection. Nucleic acid sequences complementary

to the DNA act as antisense sequences and can be used to prevent the

translation of H. pylori mRNA. Antibodies against the protein can be

used in immunoassays to evaluate the abundance and distribution of

H. pylori-specific antigens. The genomic sequence of H. pylori

(ATC 55679) as determined from overlapping contigs generated by

mechanically shearing the bacterial DNA. The sequences were analysed

for ORF of at least 180 nucleotides, and the predicted coding regions

for ORF of at least 180 nucleotides, and the predicted from various ORF

were analysed for significant homology to other known or exported

methanicallar regions can be isolated from H. pylori by PCR

interest, particular regions can be isolated from H. pylori by PCR

amplification for recombinant polypeptide production, e.g. in E. coli
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                                                                                                        activator;
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infection and for diagnosis of H. pylori infection
                                                                       envelope;
                                                               Cytoplasmic; vaccine; prevention; treatment; infection; envelope identification; binding compound; bacteria; life cycle; activato inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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H. pylori ORF 06ep30223_4698838_f2_55 inner membrane protein.
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Matches 185; Conservative 129; Mismatches 255;
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96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
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nqtffghgyygvktaslgyfkkpldkltlkeitmlvalprapsfydptknlefslsrand 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
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                                                                                                                                                                                                                                                                                                                                                      H. pylori ORF 06ep30223_4698838_f2_55 protein.
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N-PSDB; AAV24985.
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This sequence is a H. pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori
The protein may be used in a vaccine to prevent or treat H. pylori
The protein or to identify H. pylori life cycle activators or inhibitors. The
Useful as potential H. pylori life cycle activators or inhibitors. The
CDNA and probes derived from it may be used for the identification of
The pylori in a sample and the diagnosis of H. pylori infection. Nucleic
CDNA and probes complementary to the DNA act as antisense sequences and
CDNA act as antisense sequences and
CDNA action can be used in immunoassays to evaluate the abundance
CDNA addistribution of H. pylori-specific antigens. The genomic sequence of
CNATC 55679) was determined from overlapping contigs generated
CNATC 56791 was determined from overlapping contigs generated
CNATC 56791 was determined from overlapping contigs generated
CNATC 56791 was determined from overlapping regions
CNATC for ORF of at least 180 nucleotides, and the predicted coding regions
CNATC for CNATC evaluation. To identify likely H. pylori antigens for
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ilarity 28.2%; Pred. No. 4.3e-35;
Conservative 129; Mismatches 255;
Claim 14; Pages 780-781; 1145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 AA;
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Db 603 ysyfmrnilaiepslkrkfdvpkglrk--eivdkipyysspnsitp-tpkktdds 654

Search completed: June 13, 2002, 08:42:39 Job time: 125 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 13, 2002, 08:41:44; Search time 13.62 Seconds (without alignments) 1893.335 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-08-961-083-2 3484 1 KIYDNKNQLIADLGSERRVN......TQQSNTTPDQQNQNPQPAQP 666

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	moradi rosag	Q04707 streptococc	m		0		neisseria f	Q07806 pseudomonas		O05194 neisseria m	005131 neisseria g	neisseria	Q9knu5 vibrio chol		Ч	>	es		ч		Q9pgd4 xylella fas			Q07259 alcaligenes			Q03524 bacillus su	024849 acinetobact	Q9muv9 mesostigma	O52423 neisseria m	Q48465 klebsiella	22	89	P04286 escherichia
SUMMARIES		PBPA_STRPN	PBPA_STROR	PBPA_BACSU	PBPF_BACSU	PBPA_AQUAE	PBPA_NEIFL	PBPA_PSEAE	PBPA_NEILA	PBPA_NEIMA	PBPA_NEIGO	PBPA_NEICI	PBPA_VIBCH	PBPD_BACSU	PBPA_HAEIN	PBPB_VIBCH	PBPA_ECOLI	PBPB_ECOLI	PBPB_HAEIN	PBPA_RICPR	PBPA_XYLFA	PBPB_BUCAI	PBPC_ECOLI	TRG_ALCEU	PBPB_BACSU	MTGA_NEIGO	SP5D_BACSU	MTGA_ACICA	FTSI_MESVI	MTGA_NEIMA	MTGA_KLEPN	MTGA_ECOLI	MTGA_HAEIN	FTSI_ECOLI
Length DR		19			714 1																													80
% Query		•	77.5	28.7	21.2	•	19.5		18.4					17.2				15.1			14.1	13.5	12.9	9.0	5.9	5.9	5.9	5.6	5.6	5.5	5.3	5.3	5.5	4.7
000		3484	2698.5	666	739	712	680.5	642.5	640	640	635.5	633	617	598.5	591.5	584	267	526	525.5	502.5	490.5	472	450.5	312.5	207	206	206	194.5	193.5	192	185.5	83	8	164
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P38536 t amylopull P14677 streptococc P45059 haemophilus P54488 bacillus su P25054 homo sapien P13692 enterococcu Q03674 saccharomyc P39653 streptococcc P40954 candida alb	P57317 buchnera ap Q9pjt6 chlamydia m P29336 streptococc
APU_THETU PBRX_STRPN YGTS_HABIN YQGF_BACSU APC_HUMAN P54_ENTFC PLB2_YEBAST DEXT_STRDO CH13_CANAL	FTSI_BUCAI Y741_CHLMU GTFS_STRDO
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## ALIGNMENTS

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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          LOSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                               1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
                                                                                                                                                                                                                        enzyme; Complete proteome.
370 ACYLATED BY PENICILLIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                                                                                                                                                                  T -> A (IN STRAIN R6).
V -> I (IN STRAIN 83915).
D -> E (IN STRAIN R6).
E -> K (IN STRAIN 83915).
M -> I (IN STRAIN 83915).
D -> E (IN STRAIN 45607).
T -> S (IN STRAIN 45607).
N -> S (IN STRAINS 45607 AND R6).
M, 5BD397E83B4B3AAG CRC64;
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                        Length 719;
                                                                                                                                                                                                    ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Antibiotic resistance; Cell wall; Multifunctional enzyme; Complete proteome.
SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THESE STRAINS ARE PENICILLIN-SENSITIVE.
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                          Score 3484; DB 1;
Pred. No. 2.5e-193;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                            SER-RICH
                                                                                                                                                               InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PP00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase: 1.
                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                  EMBL; AE007349; AAK74536.1; -.
                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                      EMBL; X67873; CAA48073.1; -. EMBL; X67872; CAA48072.1; -.
                                                                                                                          EMBL; M90527; AAA26956.1; -.
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386
388
397
                                                                                                                                             PIR; S28038; S28038.
                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                    124
386
386
397
523
533
540
657
                                                                                                                                                       TIGR; SP0369;
                                                                                                                                                                                                                                                                                                                                                                             Matches 666;
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VARIANT
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
STWNSPAPQQPPSTESSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
                                                                                 AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92325042; PubMed=1624444;
Martin C., Briese T., Hakenbeck R.;
"Nucleotide sequences of genes encoding penicillin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Antibiotic resistance; Cell Wall;
Multifunctional enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70891 MW; A6D198BCEA603A63 CRC64;
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87.5%; Pred. No. 3.5e-148;
ive 39; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Penicillin-binding protein la (PBP-1A) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       637 AA
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InterPro; IPR001460; Transpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M90528; AAA26958.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1303;
                                                                                                                                                                                                                                               POPAOP 666
                                                                                                                                                                                                                                                                                     POPAQP 719
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PBPA_STROR
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AC Q00573;
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NON_TER
SEQUENCE
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A/1B (PBP1) [Includes: Penicillin-linching transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                 419
                                                                                                                                                                                                                                                                                                                                                                                   NVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTFVYNWD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                         DKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT 479
                                                                           LSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLL
                                                                                                                                                                                                              TTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSS
                                                                                                                                                                                                                                                                                                                                                               RGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168 / MARBURG;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Popham D.L., Setlow P., "Cloning, nucleotide sequence, and mutagenesis of the Bacillus subtilis ponA operon, which codes for penicillin-binding protein (PBP) 1 and a PBP-related factor."; J. Bacteriol. 177:326-335(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the Bacillus subtilis chromosome region b
the serA and kdg loci cloned in a yeast artificial chromosome."
Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNI 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 914 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 499-515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROWTH REQUIREMENTS. STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
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PBPA_BACSU
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DETCHINGUES OF CROSS-LINKED

- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED

- PERTIDGCLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A

PENICILLIN-INSENSITYE TRANSCLYCOSYLASE N-TERMINAL DOMAIN

(FORMATION OF LINEAR GIYCAN STRANDS) AND A PENICILLIN-SENSITYE

TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE

SUBUNITS) (BY SIMILARITY).

- SUBCELLUAR LOCATION: TYPE II MEMBRANE PROTEIN, PROBABLY FOUND ALL

OVER THE WHOLE CELL AT LOW CONCENTRATIONS. ALSO LOCALIZES TO THE

DIVISION SITE IN VECETATIVE CELLS.

- DEVELOPMENTAL STAGE: EXPRESSION IS CONSTANT DURING GROWTH,

DEVELORMENTAL STAGE: EXPRESSION IS CONSTANT DURING GROWTH,

DEVELORMENTAL STAGE: EXPRESSION IS CONSTANT DURING GROWTH

INTO SPORE GERMINATION.

- I- PTM: THE PRODUCT EXPRESSED FROM THE TRANSLATION OF THE PONA GENE

APPEARS AS TWO BANDS ON A GEL (1A AND 1B), BUT THE SPECIFIC AMINO

ACID SEQUENCE OF EACH PROTEIN IS UNKNOWN.

- I- PTM: THE N-TERMINUS IS BLOCKED.

- I- TIS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS

OF MG2+ OR CA2+ FOR GROWTH AND GERMINATION. DEPECTS.

- I- STANDARD STATIALLY ELIMINATE THE SEPTATION DEFECTS.

- I- STANDARD STATIALLY ELIMINATE THE SEPTATION DEFECTS.

- I- STANDARD STATIALLY ELIMINATE THE SEPTATION DEFECTS.

- I- STANDARD STANDARD SECTION; BELONGS TO THE

TRANSCLOCKY AND THE N-TERMINAL SECTION; BELONGS TO THE

TRANSCLOCKY AND THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ncillus subtilis cells lacking penicillin-binding protein 1 require reased levels of divalent cations for growth.";

Bacteriol. 180:4555-4563(1998).
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Hydrolase; Multifunctional enzyme; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN)
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                                                                                                                                                                                                                                                                 Pedersen L.B., Angert E.R., Setlow P.; "Septal localization of penicillin-binding protein 1 in Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
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TRANSPEPTIDASE.
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
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Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 181:3201-3211(1999).
                                                                                                                                                                                       STRAIN=168; MEDLINE=99255546; PubMed=10322023; MEDLINE=99255546; PubMed=10322023;
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                                                                                                                                                        SUBCELLULAR LOCATION.
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329
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914 AA;
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                                                              QSN-SLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                             VYMSNGNYGMQTAAQNYYG-KDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV 179
                                                                                                                                                             LSEMKNQGYISAEQYEKAVNTPITD-GLQSLK-----SASNYPAYMDNYLKEVINQVEEE 233
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                          Gaps
                                                 2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61
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Score 999; DB 1; I
Pred. No. 4.2e-50;
; Mismatches 256;
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31.2%;
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             Similarity
                         Matches 254;
   Query Match
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RESULT 4
PBPF_BACSU
STANDARD; PRT; 714 AA.
C P8BPE_BACSU
STANDARD; PRT; 714 AA.
C D1-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-1994 (Rel. 30, Last sequence update)
DF 16-OCT-2001 (Rel. 40, Last annotation update)
DF Penicillin-binding protein IF (PBP-IF).
GN PBPF OR PONA.
OS Bacillus subtilis.
OC Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Membrane-associated.
SUBCELLULAR LOCATION: Membrane-associated.
BUFCELDULAR LOCATION: Membrane-associated.
BUFCELDULAR LOCATION: Membrane-associated.
BUFCELDULAR STARESSION REMAINS CONSTANT DURING VEGETATIVE GROWTH, DECREASES DURING EARLY SPORULATION, AND IS INDUCED IN THE STAILLARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSCIPCOSYLASE FAMILY.
TRANSCIPCOSYLASE FAMILY.
TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 122-714 FROM N.A.

MEDLINE=93094140; PubMed=1459957;
Hansson M., Hederstedfi L.;
Historing and characterization of the Bacillus subtilis hemEHY gene cluster, which encodes protoheme IX biosynthetic enzymes.";
J. Bacteriol. 174:8081-8093(1992).
-: FUNCTION: CELL WALL FORMATION. MAY BE INVOLVED IN OUTGROWTH OF THE GERMINATED SPORE OR IT COULD FUNCTION IN THE SYNTHESIS OF THE GERM CELL WALL.
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08D96718C84BB434 CRC64;
                                                                                                                                the glyB marker, many genes encoding transporter proteins, and the ubiquitous hit gene.";
                                                                                                                of the
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Cell wall; Transmembrane; Signal-anchor;
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                                                                               Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt I
Wedler H., Venema G., Bron S.;
"The 172 kb prkA-addAB region S.;" afthe 172 kb prkA-addAB region S.
Bacillus subtilis chromosome contains several dysfunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
TRANSGLYCOSYLASE.
TRANSPEPTIDASE.
                                                                                                                                                                                                                                                              Poppham D.L., Setlow P.; and regulation of the "Cloning, nucleotide sequence, and regulation of the subtilis pbpr gene, which codes for a putative class high-molecular weight penicillin-binding protein."; J. Bacteriol. 175:4870-4876(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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EMBL: L10630; AAA71942.1; -.
EMBL: M97208; AAA22516.1; -.
EMBL: 299109; CAB12851.1; -.
PIR: A40614; A40614.
SubtiList; BG10428; pbpF.
InterPro: IPR001264; Transpeptdse.
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Pfam; PF00905; Transpeptidase; 1.
Probom; P0001895; Transglycosyl;
Peptidoglycan synthesis; Cell wal
Complete proteome.
                                                                MEDLINE=98240224; PubMed=9579061;
                                                                                                                                                                                                                                                  MEDLINE=93328693; PubMed=8335642;
                                                                                                                                                                                Microbiology 144:859-875(1998).
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714 AA;
NCBI_TaxID=1423;
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                         18;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-la) (PBPla) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                            416
                                                               KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV 179
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                          Gaps
                                                 1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
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 Length 714;
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Score 739; DB 1;
Pred. No. 2.7e-35;
9; Mismatches 237;
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NCBI_TaxID=63363;
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                         Conservative 119;
21.2%;
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           Best Local Similarity
Matches 187; Conserv
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 EVYDAKGRLYGTIGIQKRFYVSIDKIPEHVINAFVATEDRNFWHHGIDPVAIVRAAIVN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LQSNSL-QGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACYLATED BY PENICILLIN (BY SIMILARITY) 37F756397C9D7B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 KGRLKIYTTIDLDYQKIAQKSLEEGLKRVAKIIGLPFLPKSEEDMELAYEKEAQLKRLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 GKIYVAKILKYDGNFMKVEIHGKKLKGEIKGLNTEGHKYVFVKYLGGNRAEIIPDLEGSL
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                                                                                                                                                                                                                                                                                                           Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transglycosyl; 1.
Probom; P001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransfera Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Signal-anchor; Antiblotic resistance; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE II MEMBRANE DEFINITAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC (POTENTIAL).
TRANSGLYCOSYLASE.
TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 712; DB 1;
Pred. No. 1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 109; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 TIGMDVYINVDQE----AQKHLWD------
                                                                                                                                                                                           EMBL; AE000699; AAC06835.1; -.
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%;
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213
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726 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBPla) [Includes: Penicillin-insensitive transglycosylase (EC 24.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4..-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNITS) (BY SIMILARITY).
-1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
-1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00912; Transglycosy1; 1.
Pfam; PF00915; Transpeptidase; 1.
ProDom; PD001895; Transplycosy1; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACYLATED BY PENICILLIN (BY SIMILARITY). ODDCDF6FD25953AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the ponA gene encoding penicillin-binding protein 1 of Neisseria flavescens.";
Submitted (AUG-1988) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).

-I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSCLYCOSYLASE FAMILY.

-I- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERIPLASMIC (POTENTIAL). TRANSGLYCOSYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
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larity 25.8%; Pred. No. 7.5e-32;
Conservative 129; Mismatches 277;
                                                                                                                                             798 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPEPTIDASE
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
                                                                                                                                             PRT;
                                                                                                                                                                                          (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NRL 30009;
ROPP P.A., Nicholas R.A.;
:: ||::|
665 KVVIRMYPNEDFELP 679
                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                              Neisseria flavescens
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798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=484;
                                                                                                                                                                                                                                                                                                                                   MRCA OR PONA
                                                                                                                                                                                          16-OCT-2001
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16-OCT-2001
                                                                                                                                        PBPA_NEIFL
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ACT_SITE
SEQUENCE
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Best Local
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                                                                                                                    PBPA_NEIFL
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-101 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBP-1a) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
MRCA OR PONA OR PA5045.
                                                                                    VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                             228
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62 QSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
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PLRIAEGYSVFANGGYKVSAHVIDKIYDSQGRLRAQMQPLVAGENAPQAIDPRNAYIMYK 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671 TAVYIGFDKPRSMGRAGYGGTIAVPVWVEYIGFALKGTSVKPMKAPEGVVTNGGEVY--- 727
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                         SEMKNOGY I SAEQY EKAVNTP I TDGLQSLK SASNY PAYMDN - - - - - YLK EVINQ - VEEE
                                                                                                                                                                                                    TGYNLLTTGMDVYT
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STRAIN-ATCC 15692 / PAO1;
Handfield J., Gagnon L., Dargis M., Huletsky A.;
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Q07806;
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20;

Gaps

179;

Indels

IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61

Similarity

Matches 203;

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g ð

119

LQSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN

61

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SEQUENCE OF 1-167 FROM N.A.
SEQUENCE OF 1-167 FROM N.A.
STAIN-ATCC 15692 / PAO1:

WEDLINE-94049125; PubMed-7901733;
MATTIN P.R., Hobbs M., Free P.D., Jeske Y., Mattick J.S.;
MATTIN P.R., Hobbs M., Free P.D., Jeske Y., Mattick J.S.;
Type 4 finbriae in Pseudomonas aeruginosa.";
Type 4 finbriae in Pseudomonas aeruginosa.";
Mol. Microbiol. 9:857-868(1993).

CI- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIOGGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENICILLIN-INSENSITIVE TRANSCINCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
SUBBURITS) (BY SIMILARITY).

CI- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

CI- SUBCLIULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; P0001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane;
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DOMAIN 1 5 CYTOPLASMIC (POTENTIAL).

TRANSMEM 6 26 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                     SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSPEPTIDASE.
ACYLATED BY PENICILLIN (BY SIMILARITY).
OBIA3F6FA5D492AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-:- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSGLYCOSYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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TRANSGLYCOSYLASE.
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EMBL; L13867; AAC36826.1; -.
InterPro; IPR001264; Transglycosyl.
InterPro; IPR0010460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
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91199 N
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48
403
461
822 AA;
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PBPA_NEILA STANDARD; PRT; 798 AA.
087579;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40,
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120 KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV
                                                                                                                                                                                 237 NLLTTGMDVYTN------VDQEAQ-------KHL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 PAIVTQVEKSGIMVMTRDGKEEAVTWDSMKWARPFLSNNSMGPMPRQPADVAQAGDQIRV
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ROPP P.A., Nicholas R.A.;
*Nucleotide sequence of the ponA gene encoding penicillin-binding
protein 1 from Neisseria lactamica.";
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25;

Gaps

Indels 229;

18.4%; Score 642.5; DB 1; Length 822; 25.4%; Pred. No. 1.2e-29; Indels 229; Live 122; Mismatches 252; Indels 229;

Conservative 122;

Similarity

Query Match Local

205;

Best Loca Matches

49

g ŏ

KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Three are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD001895; Transglycosyl; 1.
Peptidodyycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Signal-anchor; Antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 QSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 VYSADGKIIGIYGEORREFTKIGDFPEVLRNAVIAAEDKRFYQHWGVDVWGVARAVVGNI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDN-----YLKEVINQ-VEEE 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 IRRGAVIRVRNNGGRWAVVQEPLLLQGALVSLDAKTGAVRALVGGYDFHSKT---FNRATQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPEPTIDASE.
ACYLATED BY PENICILLIN (BY SIMILARITY).
3B9C7672B86935D6 CRC64;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOGLYCAN FROM THE LIPID INTEREDIATES. THE ENZYME HAS A
PENICTILIN'INSENSITIVE TRANSCIPCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN'SENSITIVE
                                                                                               TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY SIMILARITY).
PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 YGEDAYTOGLKVYTTVRTDHOKAATEALRKALRNFDRGSSYRGAESYIDLGRDEDAEEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNMLEEKMITLQQRDQALNEEL------HYERFVQKIDQSALYVAEMVRQELYEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%; Score 640; DB 1; Length 798; 26.0%; Pred. No. 1.6e-29;
                                                                                                                                                                         similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSGLYCOSYLASE FAMILY.
                                                                                                                                                                                                                                   SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
PERIPLASMIC (POTENTIAL).
TRANSGLYCOSYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 126; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF085689; AAC35363.1; -. InterPro: IPR001264; Transglycosyl. InterPro: IPR001460; Transgeptdse. Pfam; PF00312; Transglycosyl; 1. Pfam; PF00905; Transpeptidase; 1.
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378
461
798 AA;
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DOMAIN
ACT_SITE
SEQUENCE
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Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
                                                                                                                                                   424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               670 VVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGRPGKGMKMPDGVVAGNGEYYM 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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binding protein 1 from Neisseria gonorrhoeae and Neisseria
meningitidis.";
J. Bacteriol. 179:2783-2787(1997).
311 TNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN-----TPVYNWDRGYFG
                                                                         455 AMRQPGSTFKPFV-YSAALSKGM--TASTMINDAPISLPGKGPNGSVWTP-KNSDGRYSG
                                                                                                                                                                                                                                                                                                              425 ASSEKWAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE-----FSNVGTRAMKETTAYMM
                                                                                                                                                                                                                                                                                                                                                                                            566 -TPLRIAEAYSVFANGGYRVSSYVIDKIYDSEGRLRAQMQPLVAGQNAPQAIDPRNAYIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 TDMMKTVLTYGTGRNA-YLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 YSMAVWTGYSN-RLIPPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYR-NGEFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 KN-----GARSTWNSPAPQQPPS-----TESSSSSSSSSSSSSTSQSSTTPSTNNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730 KEHMVTDPGLMLDNGGAAPQ--PSRRVKEDDGGAAEGGRQEADDESRQDMQETPVLPSNT
                                                                                                                                                   NITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYG
                                                                                                                                                                                                                             511 YITLRQALTASKNMVSIRILMSIGVGYAQQYIRRFGFKPSELPVSLSMALGTGET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798
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MEDLINE-20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=22491 / Serogroup A / Serot
MEDLINE=97252514; PubMed=9098083;
Ropp P.A., Nicholas R.A.;
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Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser Ç.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neissería meningitidis serogroup B strain MC58."; Science 287:1809-1815(2000).
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Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane;
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                                                                                                   PEGIOCE 287:1809-1815(2000).

-!- FUNCTION: CELL MALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZME HAS A
PENTICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPERPIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
SUBUNITS) (BY SIMILARITY).

-!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (
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InterPro: IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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- I- FUNCTION: CELL WALL FORMATION SYNTHESIS OF CROSS-LINKED
PEPTIDOGLICACIN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENTIDICLIV-INSENSITIVE TRANSCLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
SUBUNITS) (BY SIMILARITY: ESSENTAL FOR CELL WALL SYNTHESIS.

- I- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

- I- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBPIa) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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meningitidis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding
                                                                                                                                                                                                                                                                                                                                         311 INRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN~
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MEDLINE-97252514; Pubmed-9098083;
MORP P.A., Nicholas R.A.;
"Cloning and characterization of the ponA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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--HLWDIYNTDEYV
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PBPA_NEIGO
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                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
PER PLASMIC (POTENTIAL).
TRANSGIYCOSYLASE.
TRANSGIATO BY PENICILLIN (BY SIMILARITY).
ACYLATED BY PENICILLIN (BY SIMILARITY).
                                                                                                  InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transglycosyl.
Pfam; PF00912; Transglycosyl; 1.
Probom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell Wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIYNTDEYV------273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN-----TPVYNWDRGYFGNITLQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE-----FSNVGTRAMKETTAYMMTDMMK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 YTQGFKVYTTVRTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 GLYTVDKMVPAVVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEK 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMKNQGYISAEQYEKAVNTPI -- TDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 VIRVKNNGGRWAVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKT---FNRAVQAMRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAEAYSVFANGGYRVSSHVIDKIYDRDGRLRAQMQPLVAGQNAPQAIDPRNAYIMYKIMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVLTYGTGRN-AYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAV
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 207; Conservative 120; Mismatches 287; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                             Length 797;
                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                          18.2%; Score 635.5; DB 1
26.4%; Pred. No. 2.9e-29;
                                                                                                                                                                                                          Antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                     88364 MW;
                                                                                        EMBL; U72876; AAB52536.1; -
                                                                                                                                                                                                                        7880
                                                                                                                                                                                                                                                                                          217
699
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                                                                                                                                                                                                          Signal-anchor;
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DOMAIN
TRANSMEM
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBP-1a) (FBP-1a) Penicillin-insensitive transglycosylase (EC 2.4.2.) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.) (Poptidoglycan TGase)].
                     597
                                                                                                             734 TDPGLMLDNSGIAPQ--PSRRAKEDDEAAVENEQQGRSDETRQDVQETP---VLPSNTDS 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria cinerea.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CIONING and Sequence analysis of the ponA gene encoding penicillin binding procein I from Neisseria cinerea."

Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDGOLYCAN FROM THE LIPPID INTERNEDIATES. THE ENYTHE HAS A PENICILLIN-INSENSITIVE TRANSCINCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACYLATED BY PENICILLIN (BY SIMILARITY) 5842ED4BCB9FF06A CRC64;
WTGYSN-RLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLY-RNGEFVFKN---
                                                                          ---GARSTWNSPAPQQPPSTESSSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSCINCOSTALESE FAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD001895; Transglycosyl; 1.
Probom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell Wall; Transferase; Glycosy Hydrolase; Multifunctional enzyme; Transmembrane; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERIPLASMIC (POTENTIAL).
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TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                      AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001264; Transglycosyl.
Interpro; IPR001460; Transgptdase.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
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218 TH
700 TH
461 AC
87843 MW;
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ROPP P.A., Nicholas R.A.;
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
50
414
461
798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
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086088;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBP-1a) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.) (DD-transpeptidase)].
                                                                            QSNSLQ-GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                                         337
                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                                                                    397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 TNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYP--GTNTPVY---NWDRGYFGN 365
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                               Gaps
                                                         2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61
                                                                                                                                      278 YGEDAYTQGFKVYTTVRTDHQKVATEALRKALRNFDRGSSYRGAESYIDLSKGEDVEETV
                                                                                                                                                                                                                                                                                                                                                                                                  338 SQYLSGLYTVDKMVPAIVLDVTKRKNVVIQLPSGKRVTLDGRSLGFAARAVNNEKMGESR
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512 ITLRQALTASKNMVSIRILMSIGVGYAHEYIQRFGFKPSELPASLSMALGTGET-----
                                                                                                                                                                                                              IYLGQRAYGFASAAQIYFNKDVRELTLAEVAMLAGLPKAPSAYNPIVNPERAKLRQKYIL
                                                                                                                                                                                                                                            SEMKNOGY I SAEQY EKAVNTPITDGLQSLKSASNY PAYMDN-----YLKEVINQ-VEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 IRRGSVIRVRNNGGRWVVVQEPLLQATLVSLDAKTGAVRALVGGYDFHSKT---FNRAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE-----FSNVGTRAMKETTAYMMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLKIAEAYSVFANGGYRVSSHVIDKIYGSDGRLRAQMQPLVAGQNAPQAIDPRNAYIMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMMKTVLTYGTGRN-AYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 KIMQDVVRVGTARGAAALGRSDIAGKTGTTN-----DN------KDAWFVGFNPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMAVWTGYSN-RLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLY-RNGEFVFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671 VTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGGOGKGMKVPEGVVSSNGEYYMK
                              Indels 166;
Length 798;
                            Conservative 115; Mismatches 248;
                                                                                                                                                                                                                                                                                                                                                                     --HLWDIYNTDE------
               4.1e-29;
 DB 1;
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                                                                                                                                                                                                                                                                                                         TGYNLLTTGMDVYTNVDQEAQK------
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Score 633;
Pred. No. 4
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STRAIN-EL TOR N16961 / SEROTYPE Ol,
MEDLINE=20406833; Pubmed=10952301;
18.2%;
26.5%;
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              Similarity
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                            Matches 191;
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Q9KNU5;
Query Match
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                                                                                                                                                                         -:- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOGLYCAN FROM THE LIPID INTEREMEDIATES. THE EXZYME HAS A
PENICILLIN-INSENSITIVE TRANSCRIVCOSYLASE N-TERMINAL DOMAIN
FORMATION OF LINEAR GIYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
SUBUNITS) (BY SIMILARITY).
-:- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001264; Transglycosyl.
Pfam: PF00912: Transglycosyl: 1.
Probom, PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Signal-anchor; Antibiotic resistance; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACYLATED BY PENICILLIN (BY SIMILARITY).
8A9553DA2650B9D2 CRC64;
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                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 825;
                                                                                                                                                                                                                                                                                                                                                        TRANSGLYCOSYLASE FAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                        : IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERIPLASMIC (POTENTIAL).
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llarity 24.3%; Pred. No. 3.6e-28;
Conservative 128; Mismatches 220
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Nature 406:477-483(2000).
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Best Local Simi
Matches 200;
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                                                                                                                                                                                                                                                                                                      ---NRLTPLVGN 556
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                                                                                                                                  G-----YFGNITLQYALQOSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIH 407
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S12; ALSO KNOWN AS THE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 2 FAMILY.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                              ----DETO----
                                                 ----VASTIVDVSNGKVIAQLGARHOSSN
                                                                   SANEFLAAGQQIWVRPRTQDGAITAWKLTQVPNANTAFVAMNPENGAVTALVGGFNFVHN
                                                                                        301 VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                             ---KFNRATQSVRQVGSSIKPFI-YSAALNKGL--TLATLINDAPIN------QWDE
                                                                                                                                                                          408 YSNAISSNTTESDKKYGASS---EKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSN
                                                                                                                                                                                                                                                            490 -TGRNAYLAWLPQA------GKTGTSNYT----------------------------DEEIENHIKT
                            338 SEYLSNEPTYGDMFPAAVLSVEEKSAOVWVKSYGVQTIAWEDMNWARRFINDDRQGPLPK
                                                                                                                                                                                                                                       608 IEFSAEPKVVCHRECSSELDEFAEQDAASPYAPKVISEQNAFLTREMLYSNIWGGGEWSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Popham D.L., Setlow P.; "Cloning, nucleotide sequence, mutagenesis, and mapping of the Bacillus subtilis pbpD gene, which codes for penicillin-binding
                                                                                                                                                                                                                                                                                                                                                          557 GLTVAAKVYRSMMTYLSEGSNPEDW---NIPEGLY--RNGEFVF 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firm.cutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
         --YVAYPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 4 precursor (PBP 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 317-331.
                                                                                                                                                                                                                                                                                                                                                                                                                     624 AA
                                                                                                                                                                                                                                                                                                    522 --SQFVAPDELFAGYTRKYSMAVWTGYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 176:7197-7205(1994).
                                                                                                                                                                                                                                                                                                                                                                                                         D_BACSU STANDALL.
PBPD_BACSU STANDALL.
PAD70750; 005232; 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seque:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95050302; PubMed=7961491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
         --YNTDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NLQSNSL-QGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------LLTTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 QVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : ::: ::|| | :: CGGAAVINHQTHQIIALSGGKNYQ---KYDFNRAYQAYRQPGSSIKPLLDYGPYIEQTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 FLNGLGIDYPSIHYSNAISSN----TTESDKKYGASSEKMAAAYAAFANGGTYYKKPMYIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 YIE-----PYHFAKLVDSDYLLPAALGGFTNGMTPLEMTKAYTTFGNSGSYTPSHAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 KVVFSDGSE-KEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
PENICILLIN-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACYLATED BY PENICILLIN (BY BOE6BD4B4EC7ACE4 CRC64;
                                                                                                                                                                                                                                                          Subtliist; BG1097; pppD.
InterPro; 1PR001264; Transglycosyl.
Fam; PF00127; Transglycosyl.
Pfam; PF0012; Transglycosyl; 1.
Pfam; PF0012; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell Wall; Signal; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.2%; Score 598.5; DB 1; Best Local Similarity 26.9%; Pred. No. 2.7e-27; Matches 159; Conservative 117; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM.
                                                                                                                                                                                            EMBL; U11882; AAA64943.1; -. EMBL; Z93933; CAB07915.1; -. EMBL; Z99120; CAB15138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 21
22 624
388 388
624 AA; 70625 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Langen H., Takacs B. Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M.;

Gray C., Fountoulakis M.;

Two-dimensional map of the protecome of Haemophilus influenzae.";

Electrophoresis 21:411-429(2000).

-!- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PERTIDGCLYCAN FROM THE LIPID INTERMEDIATES. THE BRYZME HAS A PENICILLIN INSENSITIVE TRANSGLYCOSYLASD N-FERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY SIMILARITY).

-!- PATHWAY: FIRAL STRAGES IN PEPTIDGGLYCAN SYNTHESIS.

-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RD / KW20 / ATCC 51907;

MEDLINE=9350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharma U.K., Dwarakanath P., Banerjee N., Town C., Balganesh T.S.; "Expression and characterization of the ponA (ORF I) gene of Haemophilus influenzae: functional complementation in a heterologous
                                                          01-JUL-1993 (Rel. 26, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBP1a) (Penicillin-binding protein A) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.) (Peptidoglycan TGase); Penicillin-sensitive transpeptidase (EC 3.4...) (Db-transpeptidase)
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomb J.-F., El-Hajl H., Smith H.O.;
"Nucleotide sequence of a cluster of genes involved in the transformation of Haemophilus influenzae Rd.";
Gene 104:1-10(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
853 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION BY MASS SPECTROMETRY.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 177:6745-6750(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=92009183; PubMed=1916268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20137488; PubMed=10675023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=96074300; Pubmed=7592463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995).
STANDARD;
                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 AVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASS---EKMAAAYAA 436
                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                              Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LGAASFTPLEMARAYAV 554
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGA-FLR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VSFG----VSFG------INQAVETNRDWGSTMKPITDYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 ALEYGVYDSTATIVHDEPYNY--PG-----TNTPVYNWDRGYFGNITLQYALQQSRNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSGYKVFTTVLSKDQAEAQKAVRNNLIDYDMRHGYRGGAPLWQKNEAAWDNDRIVGFLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 LPDSEPFIPAAVIGIVKGGADILLASGEKMTLSTNAMRWTGRSNPVKVGEQIWIHQRANG
                                                                                                                             Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
Protom: P001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransfer: Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Signal-anchor; Antibiotic resistance; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 LSRMLDEKYISKEEYDAALKEPIVASYHGAKFEFRADYVTEMVRQEMVRRFGEENAY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TTGMDVYTNV---DQ-EAQK--------HLWD----IYNTDEYVAY---
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                       Length 853;
                                                                                                                                                                                                                                                                                                                         -> LPSVETLKTVEL (IN REF. 1). FC0846096CDB663B CRC64;
                                                                                                                                                                                                                                                                                                              ACYLATED BY PENICILLIN (BY
                                                                                                                                                                                                                                                                   PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 591.5; DB 1; 29.2%; Pred. No. 1.1e-26; ive 99; Mismatches 176;
                                                                                                                                                                                                                                                                                 TRANSGLYCOSYLASE.
                                                                                                                                                                                                                                                                                                TRANSPEPTIDASE
                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 AIRAIQTAGIDFTAEFLORFGFKRDOYFASEALA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 -PDDELQVASTIVDVSNG--KVIAQLGAR---
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                                                                                                  InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
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                                                                                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                            33
94221
                                           EMBL; M62809; AAA25007.1;
                                                       EMBL; U32727; AAC22099.1;
PIR; JH0438; JH0438.
TIGR; H10440; -.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.23
Matches 166; Conservative
                                                                                                                                                                                                                                                                 853
205
681
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37
387
441
33
853 AA;
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CONFLICT
                                                                                                                                                                                                                                       TRANSMEM
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 406:477-483(2000).

-I FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOCLICACIN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENIZILLIN-INSENSITIVE TRANSCLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENIZILLIN-SENSITIVE
TRANSPEPPITIDASE C.-PERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
SUBBUNITS) (BY SINILARITY).

-I- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

-I- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                      STRAIN-EL TOR NIG961 / SEROTYPE 01;
MEDLINE-20406833; Pubbled=10952301;
Heldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam I.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane; Signal-anchor; Antibiotic resistance; Complete protecome.

OMANN 1 30 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSPEPTIDASE.
ACYLATED BY PENICILLIN (BY SIMILARITY).
BCFC2676EA2AFFIC CRC64;
                                                    16-OCT-2001 (Rel. 40, Last sequence update)
LeCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1B (PBP-1b) (PBPlb) (Murein polymerase)
[Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.)
(Peptidoglycan Tasse); Penicillin-sensitive transpeptidase
(EC 3.4...) (DD-transpeptidase)].
                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSGINCOSTASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERIPLASMIC (POTENTIAL). TRANSGLYCOSYLASE.
  777 AA
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PRT;
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                                           131 QTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQGYIS
                                                                                                   250 DQEAQKHLWDIYNTD--EYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQ
                                                                                                                                                                                                                      308 AVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN----TPVYNWDRGYF
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                            QLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYMSNGN----YGM
                                                                                                                                            191 AEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNL-LTTGMDVYTNV
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Conservative 117;

Similarity

Matches 175;

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Query Match

Best Local

21;

Gaps

26;

16.8%; Score 584; DB 1; Length 777; 29.7%; Pred. No. 2.6e-26; rative 117; Mismatches 241; Indels

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